



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 148556

TO: Nita M Minnifield
Location: REM/3C01/3C18
Art Unit: 1645
Thursday, March 31, 2005

Case Serial Number: 09/124280

From: Toby Port
Location: Biotech-Chem Library
REM1-A59
Phone: 272-2523
toby.port@uspto.gov

Search Notes

Dear Examiner Minnifield,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

From: Pak, Michael
Sent: Tuesday, March 22, 2005 3:52 PM
To: STIC-Biotech/ChemLib
Cc: Minnifield, Nita
Subject: FW: sequence search approval needed for 09/124280

Dear Stic,

Please search the multiple sequence search request set forth below.

Thanks,

Mike Pak

-----Original Message-----

From: Minnifield, Nita
Sent: Tuesday, March 22, 2005 2:54 PM
To: Pak, Michael
Subject: sequence search approval needed for 09/124280

Michael,

I have an application that I inherited several years ago from an examiner that left the office. The previous examiner had all (41) of these sequences searched. By the time I got the case applicant had already received at least two Office Actions with all of these sequences examined. Now it is time to allow and I need approval to have an interference search done. They are all amino acid sequences, 6-13 aa/sequence.

I would appreciate approval to have an interference sequence search done on SEQ ID NO: 1, 4-19, 21-28, 30-45 of this application.

Thanks,
Minnifield
71976
Art Unit 1645
Office REM-3C01
Mailbox REM-3C18
571-272-0860

RECEIVED
MAR 22 2005
STIC

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

GenCore version 5.1.6
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OM protein - protein search, using BW model

Run on: March 26, 2005, 13:47:57 / Search time 46 Seconds
(without alignments)
79.176 Million cell updates/sec

Title: US-09-124-280A-45

Perfect score: 64
Sequence: 1 RRLKKYKXGK 11

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database:

Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*

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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*

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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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7	61	95.3	101	9	US-09-109-175-5
8	61	95.3	101	14	US-10-241-173-5
9	61	95.3	105	9	US-09-109-175-2
10	61	95.3	105	14	US-10-241-173-2
11	46	71.9	76	15	US-10-424-599-261856
12	46	71.9	222	15	US-10-424-599-220516
13	46	71.9	298	15	US-10-424-599-168507

14	68.8	16	14	US-10-271-343-54	Sequence 54, App1
15	67.2	139	15	US-10-264-237-1594	Sequence 1594, App
16	67.2	237	10	US-09-809-391-418	Sequence 418, App
17	67.2	237	10	US-09-882-171-418	Sequence 418, App
18	67.2	237	15	US-10-164-861-418	Sequence 418, App
19	67.2	297	15	US-10-424-599-275411	Sequence 275411, App
20	67.2	652	14	US-10-317-832-107	Sequence 107, App
21	67.2	761	14	US-10-317-832-14	Sequence 14, App1
22	65.6	302	15	US-10-424-599-176897	Sequence 176897, App
23	65.6	307	15	US-10-424-599-177211	Sequence 177211, App
24	65.6	661	17	US-10-104-047-2569	Sequence 2569, App
25	65.6	661	17	US-10-741-600-1621	Sequence 1621, App
26	64.1	290	16	US-10-767-701-44699	Sequence 44699, App
27	64.1	290	15	US-10-425-114-54991	Sequence 54991, App
28	64.1	338	15	US-09-833-245-190	Sequence 190, App
29	64.1	338	15	US-10-424-599-261671	Sequence 261671, App
30	64.1	346	15	US-10-424-599-259553	Sequence 259553, App
31	64.1	1020	16	US-10-437-963-131231	Sequence 131231, App
32	62.5	29	14	US-10-029-386-32465	Sequence 32465, App
33	62.5	93	15	US-10-425-114-57226	Sequence 57226, App
34	62.5	125	16	US-10-767-701-57242	Sequence 57242, App
35	62.5	273	16	US-10-437-963-190100	Sequence 190100, App
36	62.5	291	16	US-10-437-963-145297	Sequence 145297, App
37	62.5	319	15	US-10-425-114-59761	Sequence 59761, App
38	62.5	343	15	US-10-425-114-40924	Sequence 40924, App
39	62.5	357	15	US-10-425-114-57270	Sequence 57270, App
40	62.5	395	15	US-10-425-114-70295	Sequence 70295, App
41	62.5	406	16	US-10-437-963-125874	Sequence 125874, App
42	62.5	420	15	US-10-425-114-54478	Sequence 54478, App
43	62.5	422	16	US-10-437-963-116654	Sequence 116654, App
44	62.5	435	16	US-10-437-963-110656	Sequence 110656, App
45	62.5	460	15	US-10-425-114-50342	Sequence 50342, App
46	62.5	466	15	US-10-425-114-69635	Sequence 69635, App
47	62.5	745	15	US-10-425-114-57871	Sequence 57871, App
48	62.5	1046	15	US-10-425-114-57950	Sequence 57950, App
49	62.5	1148	16	US-10-437-963-111298	Sequence 111298, App
50	62.5	2222	17	US-10-684-141-4	Sequence 4, App1
51	62.5	449	15	US-10-810-486-4	Sequence 4, App1
52	60.9	499	15	US-10-369-499-3504	Sequence 3504, App
53	60.9	1004	15	US-10-114-270-32	Sequence 32, App1
54	60.9	2004	14	US-10-331-061-9	Sequence 31, App1
55	60.9	2029	15	US-10-087-684-38	Sequence 38, App1
56	60.9	2029	15	US-10-087-684-38	Sequence 38, App1
57	60.9	2037	15	US-10-218-779-39	Sequence 39, App1
58	60.9	2037	15	US-10-087-684-39	Sequence 39, App1
59	59.4	14	16	US-10-218-779-39	Sequence 39, App1
60	59.4	63	15	US-10-469-060-1177	Sequence 1177, App
61	59.4	104	15	US-10-424-599-153027	Sequence 153027, App
62	59.4	150	14	US-10-424-599-279441	Sequence 279441, App
63	59.4	150	14	US-10-138-505-36	Sequence 36, App1
64	59.4	150	15	US-10-257-864A-94	Sequence 94, App1
65	59.4	150	15	US-10-221-311-99	Sequence 99, App1
66	59.4	150	15	US-10-399-518-133	Sequence 123, App
67	59.4	216	9	US-09-815-242-13375	Sequence 13375, App
68	59.4	216	15	US-10-282-122A-73827	Sequence 73827, App
69	59.4	245	17	US-10-472-928-838	Sequence 838, App
70	59.4	293	16	US-10-437-963-151329	Sequence 151329, App
71	59.4	293	15	US-10-424-599-184005	Sequence 184005, App
72	59.4	333	15	US-10-363-616-338	Sequence 338, App
73	59.4	333	17	US-10-482-028-14	Sequence 14, App
74	59.4	333	14	US-10-106-696-6180	Sequence 6180, App
75	59.4	373	15	US-10-264-049-3049	Sequence 3049, App
76	59.4	527	9	US-09-862-678-2	Sequence 166, App
77	59.4	527	13	US-09-981-353-166	Sequence 353, App
78	59.4	527	14	US-10-052-586-522	Sequence 522, App
79	59.4	527	14	US-10-174-590-522	Sequence 522, App
80	59.4	527	14	US-10-176-759-522	Sequence 522, App
81	59.4	527	14	US-10-175-733-522	Sequence 522, App
82	59.4	527	14	US-10-174-581-522	Sequence 522, App
83	59.4	527	14	US-10-176-481-522	Sequence 522, App
84	59.4	527	14	US-10-176-749-522	Sequence 522, App
85	59.4	527	14	US-10-176-914-522	Sequence 522, App
86	59.4	527	14	US-10-176-915-522	Sequence 522, App
87	59.4	527	14	US-10-173-706-522	Sequence 522, App

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 12:25:26 ; Search time 45 Seconds

(without alignments)

18.248 Million cell updates/sec

Title: US-09-124-280A-45

Perfect score: 64

Sequence: 1 KRLLKWKYKGF 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.rep.*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.rep.*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.rep.*
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- 5: /cgn2_6/ptodata/1/1aa/PTCTUS.COMB.rep.*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.rep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	64	100.0	102	4	US-08-760-903-1
6	64	100.0	102	4	US-08-483-191-1
7	64	100.0	102	5	PCT-US96-10227-1
8	61	95.3	19	3	US-08-477-778-15
9	61	95.3	22	3	US-09-160-309-1
10	61	95.3	22	3	US-08-477-778-8
11	61	95.3	22	4	US-09-691-500-1
12	61	95.3	101	1	US-08-264-244-1
13	61	95.3	101	1	US-08-478-689-1
14	61	95.3	101	1	US-08-476-940-1
15	61	95.3	101	1	US-08-704-872-1
16	61	95.3	101	1	US-08-577-464-2
17	61	95.3	101	3	US-08-967-038-1
18	61	95.3	101	3	US-08-871-600A-1
19	61	95.3	105	1	US-08-264-244-3
20	61	95.3	105	1	US-08-478-689-3
21	61	95.3	105	1	US-08-476-940-3
22	61	95.3	105	1	US-08-704-872-3
23	61	95.3	105	1	US-08-967-038-3
24	61	95.3	105	3	US-08-871-600A-3
25	59	92.2	11	1	US-08-366-953A-25
26	48	75.0	221	4	US-09-489-039A-13704
27	43	67.2	237	4	US-09-149-476-418

28	42	65.6	661	4	US-09-949-016-6157	Sequence 6157, Ap
29	42	65.6	665	4	US-09-949-016-10776	Sequence 10776, A
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35	39	60.9	2004	4	US-09-331-899-9	Sequence 9, Appl1
36	38	59.4	78	4	US-09-513-999C-7261	Sequence 7261, Ap
37	38	59.4	216	4	US-09-583-110-4675	Sequence 4675, Ap
38	38	59.4	218	4	US-09-107-433-3679	Sequence 3679, Ap
39	38	59.4	331	4	US-09-949-016-9528	Sequence 9528, Ap
40	37	57.8	84	4	US-09-134-000C-3655	Sequence 3655, Ap
41	37	57.8	210	4	US-09-248-796A-15869	Sequence 15869, A
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57	35	54.7	777	4	US-09-531-899-921	Sequence 921, Appl
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59	34	53.1	25	1	US-07-921-178A-16	Sequence 16, Appl1
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61	34	53.1	51	4	US-09-079-030-84	Sequence 84, Appl1
62	34	53.1	107	3	US-08-654-482-6	Sequence 5, Appl1
63	34	53.1	107	3	US-08-654-482-6	Sequence 6, Appl1
64	34	53.1	108	3	US-08-654-482-1	Sequence 1, Appl1
65	34	53.1	108	3	US-08-654-482-2	Sequence 2, Appl1
66	34	53.1	136	4	US-09-513-999C-5424	Sequence 5424, Ap
67	34	53.1	139	4	US-09-270-767-40371	Sequence 40371, A
68	34	53.1	139	4	US-09-270-767-55587	Sequence 55587, A
69	34	53.1	217	4	US-09-949-016-6509	Sequence 6509, Ap
70	34	53.1	228	4	US-09-949-016-9719	Sequence 9719, Ap
71	34	53.1	233	4	US-09-949-016-8117	Sequence 8117, Ap
72	34	53.1	239	4	US-09-252-991A-16620	Sequence 16620, A
73	34	53.1	259	4	US-09-328-352-7755	Sequence 7755, Ap
74	34	53.1	261	4	US-09-489-039A-7997	Sequence 7997, Ap
75	34	53.1	280	3	US-09-134-001C-4044	Sequence 4044, Ap
76	34	53.1	282	4	US-09-502-540-15020	Sequence 15020, A
77	34	53.1	367	3	US-09-166-205B-68	Sequence 68, Appl1
78	34	53.1	372	2	US-09-806-658-4	Sequence 4, Appl1
79	34	53.1	372	2	US-08-501-003A-12	Sequence 12, Appl1
80	34	53.1	379	4	US-09-079-030-81	Sequence 81, Appl1
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82	34	53.1	389	2	US-08-501-003A-11	Sequence 11, Appl1
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84	34	53.1	391	1	US-08-103-445-5	Sequence 5, Appl1
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86	34	53.1	391	2	US-08-501-003A-13	Sequence 13, Appl1
87	34	53.1	391	2	US-08-501-003A-16	Sequence 16, Appl1
88	34	53.1	391	4	US-09-275-252A-13	Sequence 13, Appl1
89	34	53.1	391	4	US-09-949-016-5904	Sequence 5904, Ap
90	34	53.1	393	4	US-09-230-371A-29	Sequence 29, Appl1
91	34	53.1	397	4	US-09-252-991A-22719	Sequence 22719, A
92	34	53.1	398	2	US-08-501-003A-15	Sequence 15, Appl1
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94	34	53.1	425	3	US-09-230-371A-30	Sequence 30, Appl1
95	34	53.1	439	4	US-09-949-016-11483	Sequence 11483, A
96	34	53.1	450	2	US-08-611-280-2	Sequence 2, Appl1
97	34	53.1	450	2	US-08-611-280-25	Sequence 25, Appl1
98	34	53.1	450	3	US-09-195-940-2	Sequence 2, Appl1
99	34	53.1	450	3	US-09-195-940-25	Sequence 25, Appl1
100	34	53.1	450	3	US-09-562-466-2	Sequence 2, Appl1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 12:17:20 ; Search time 43.6021 Seconds

(without alignments)
75.937 Million cell updates/secTitle: US-09-124-280A-44
Perfect score: 1 KMAQKRFLLK 10Scoring table: BLOSUM62
Gapop 10.0 , Gapexc 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
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- 20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	55	100.0	10 9 US-09-765-527-8	Sequence 8, App1
2	55	100.0	10 9 US-09-124-280A-27	Sequence 27, App1
3	55	100.0	10 9 US-09-124-280A-44	Sequence 44, App1
4	55	100.0	10 15 US-10-446-628-8	Sequence 8, App1
5	55	100.0	10 15 US-10-319-786-8	Sequence 8, App1
6	55	100.0	12 9 US-09-765-527-125	Sequence 125, App
7	55	100.0	13 14 US-10-131-686A-30	Sequence 30, App1
8	55	100.0	14 9 US-09-765-527-123	Sequence 123, App
9	55	100.0	14 14 US-10-131-686A-37	Sequence 37, App1
10	55	100.0	14 15 US-10-446-628-164	Sequence 164, App
11	55	100.0	15 9 US-09-765-527-2	Sequence 2, App1
12	55	100.0	15 9 US-09-765-527-9	Sequence 9, App1
13	55	100.0	15 9 US-09-765-527-16	Sequence 16, App1

14	55	100.0	15 9 US-09-765-527-17	Sequence 17, App1
15	55	100.0	15 9 US-09-765-527-18	Sequence 18, App1
16	55	100.0	15 9 US-09-765-527-19	Sequence 19, App1
17	55	100.0	15 9 US-09-765-527-20	Sequence 20, App1
18	55	100.0	15 15 US-10-446-628-7	Sequence 7, App1
19	55	100.0	15 15 US-10-446-628-16	Sequence 16, App1
20	55	100.0	15 15 US-10-446-628-17	Sequence 17, App1
21	55	100.0	15 15 US-10-446-628-18	Sequence 18, App1
22	55	100.0	15 15 US-10-446-628-19	Sequence 19, App1
23	55	100.0	15 15 US-10-446-628-20	Sequence 20, App1
24	55	100.0	15 15 US-10-446-628-49	Sequence 49, App1
25	55	100.0	15 15 US-10-446-628-51	Sequence 51, App1
26	55	100.0	15 15 US-10-319-786-7	Sequence 7, App1
27	55	100.0	15 15 US-10-319-786-16	Sequence 16, App1
28	55	100.0	15 15 US-10-319-786-17	Sequence 17, App1
29	55	100.0	15 15 US-10-319-786-18	Sequence 18, App1
30	55	100.0	15 15 US-10-319-786-19	Sequence 19, App1
31	55	100.0	15 15 US-10-319-786-20	Sequence 20, App1
32	55	100.0	15 15 US-10-319-786-64	Sequence 64, App1
33	55	100.0	15 15 US-10-319-786-63	Sequence 63, App1
34	55	100.0	15 15 US-10-319-786-71	Sequence 71, App1
35	55	100.0	16 9 US-09-765-527-59	Sequence 59, App1
36	55	100.0	16 15 US-10-446-628-9	Sequence 9, App1
37	55	100.0	16 15 US-10-319-786-9	Sequence 9, App1
38	55	100.0	16 15 US-10-319-786-51	Sequence 51, App1
39	55	100.0	17 9 US-09-765-527-66	Sequence 66, App1
40	55	100.0	17 15 US-10-446-628-10	Sequence 10, App1
41	55	100.0	17 15 US-10-446-628-66	Sequence 66, App1
42	55	100.0	17 15 US-10-446-628-68	Sequence 68, App1
43	55	100.0	17 15 US-10-319-786-10	Sequence 10, App1
44	55	100.0	17 15 US-10-319-786-64	Sequence 64, App1
45	55	100.0	17 15 US-10-319-786-68	Sequence 68, App1
46	55	100.0	19 15 US-10-609-515-9	Sequence 9, App1
47	55	100.0	20 9 US-09-765-527-7	Sequence 7, App1
48	55	100.0	20 9 US-09-765-527-47	Sequence 47, App1
49	55	100.0	20 9 US-09-765-527-48	Sequence 48, App1
50	55	100.0	20 15 US-10-446-628-54	Sequence 54, App1
51	55	100.0	20 15 US-10-446-628-57	Sequence 57, App1
52	55	100.0	20 15 US-10-446-628-58	Sequence 58, App1
53	55	100.0	20 15 US-10-446-628-150	Sequence 150, App
54	55	100.0	20 15 US-10-446-628-151	Sequence 151, App
55	55	100.0	20 15 US-10-319-786-54	Sequence 54, App1
56	55	100.0	21 15 US-10-319-786-57	Sequence 57, App1
57	55	100.0	21 15 US-10-319-786-58	Sequence 58, App1
58	55	100.0	24 9 US-09-765-527-31	Sequence 31, App1
59	55	100.0	24 15 US-09-765-527-70	Sequence 70, App1
60	55	100.0	24 15 US-10-446-628-52	Sequence 52, App1
61	55	100.0	24 15 US-10-446-628-70	Sequence 70, App1
62	55	100.0	24 15 US-10-319-786-52	Sequence 52, App1
63	55	100.0	24 15 US-10-319-786-70	Sequence 70, App1
64	55	100.0	25 9 US-09-765-527-110	Sequence 110, App
65	55	100.0	25 9 US-09-765-527-116	Sequence 116, App
66	55	100.0	25 15 US-10-446-628-55	Sequence 55, App1
67	55	100.0	25 15 US-10-319-786-55	Sequence 55, App1
68	55	100.0	26 9 US-09-765-527-11	Sequence 11, App1
69	55	100.0	26 9 US-09-765-527-115	Sequence 115, App1
70	55	100.0	26 15 US-10-446-628-65	Sequence 65, App1
71	55	100.0	26 15 US-10-319-786-65	Sequence 65, App1
72	55	100.0	27 9 US-09-765-527-3	Sequence 3, App1
73	55	100.0	27 14 US-10-131-433-5	Sequence 5, App1
74	55	100.0	27 15 US-10-300-083-31	Sequence 31, App1
75	55	100.0	27 15 US-10-446-628-11	Sequence 11, App1
76	55	100.0	27 15 US-10-319-786-11	Sequence 11, App1
77	55	100.0	29 9 US-09-765-527-64	Sequence 64, App1
78	55	100.0	29 15 US-10-446-628-53	Sequence 53, App1
79	55	100.0	29 15 US-10-319-786-53	Sequence 53, App1
80	55	100.0	30 9 US-09-765-527-117	Sequence 117, App
81	55	100.0	30 15 US-10-446-628-149	Sequence 149, App
82	55	100.0	31 9 US-09-765-527-154	Sequence 154, App
83	55	100.0	33 14 US-10-300-083-5	Sequence 5, App1
84	55	100.0	33 14 US-10-300-083-6	Sequence 6, App1
85	55	100.0	33 14 US-10-300-083-10	Sequence 10, App1
86	55	100.0	35 14 US-10-131-686A-18	Sequence 18, App1

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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:54:27 ; Search time 17.043 Seconds
(without alignments)

43.800 Million cell updates/sec

Title: US-09-124-280A-44
Perfect score: 55
Sequence: 1 KMKRQKRFPLK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database : Issued Parents AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	10	1	US-08-311-611A-8
2	55	100.0	10	1	US-08-372-783-8
3	55	100.0	10	1	US-08-372-105-8
4	55	100.0	10	1	US-08-097-830E-27
5	55	100.0	10	1	US-08-306-473A-8
6	55	100.0	10	1	US-08-209-762-8
7	55	100.0	10	1	US-08-473-34A-8
8	55	100.0	10	1	US-08-218-026-6
9	55	100.0	10	2	US-08-653-632-6
10	55	100.0	10	2	US-08-456-112B-27
11	55	100.0	10	2	US-08-456-112B-44
12	55	100.0	10	2	US-08-621-803-8
13	55	100.0	10	2	US-08-485-445A-8
14	55	100.0	10	3	US-09-119-263-8
15	55	100.0	10	3	US-08-657-162-8
16	55	100.0	10	3	US-09-224-480-8
17	55	100.0	10	3	US-09-093-539-8
18	55	100.0	10	3	US-09-217-352-8
19	55	100.0	10	4	US-09-790-230-8
20	55	100.0	10	4	US-09-689-097-10
21	55	100.0	10	5	PCT-US94-02465-8
22	55	100.0	10	5	PCT-US95-00498-8
23	55	100.0	10	5	PCT-US95-00656-8
24	55	100.0	11	1	US-08-218-026-7
25	55	100.0	11	1	US-08-218-026-7
26	55	100.0	11	2	US-08-653-632-7
27	55	100.0	11	2	US-08-653-632-26

28	55	100.0	11	2	US-08-760-903-4	Sequence 4, Appl
29	55	100.0	11	4	US-08-482-191-4	Sequence 4, Appl
30	55	100.0	11	5	PCT-US96-10227-4	Sequence 4, Appl
31	55	100.0	12	1	US-08-311-611A-227	Sequence 227, App
32	55	100.0	12	1	US-08-372-783-227	Sequence 227, App
33	55	100.0	12	1	US-08-372-105-227	Sequence 227, App
34	55	100.0	12	1	US-08-218-026-25	Sequence 25, Appl
35	55	100.0	12	1	US-08-218-026-40	Sequence 40, Appl
36	55	100.0	12	2	US-08-653-632-25	Sequence 25, Appl
37	55	100.0	12	2	US-08-653-632-40	Sequence 40, Appl
38	55	100.0	12	2	US-08-621-803-125	Sequence 125, App
39	55	100.0	12	3	US-09-119-263-227	Sequence 227, App
40	55	100.0	12	3	US-08-657-162-227	Sequence 227, App
41	55	100.0	12	3	US-09-217-352-125	Sequence 125, App
42	55	100.0	12	4	US-08-477-778-3	Sequence 3, Appl
43	55	100.0	12	4	US-09-689-097-224	Sequence 224, App
44	55	100.0	12	5	PCT-US95-00498-227	Sequence 227, App
45	55	100.0	12	5	PCT-US95-00656-227	Sequence 227, App
46	55	100.0	13	1	US-08-261-660A-30	Sequence 30, Appl
47	55	100.0	13	1	US-08-218-026-8	Sequence 8, Appl
48	55	100.0	13	2	US-08-653-632-8	Sequence 8, Appl
49	55	100.0	13	2	US-09-280-909A-30	Sequence 30, Appl
50	55	100.0	13	5	PCT-US94-06931-30	Sequence 30, Appl
51	55	100.0	14	1	US-08-311-611A-164	Sequence 164, App
52	55	100.0	14	1	US-08-372-783-164	Sequence 164, App
53	55	100.0	14	1	US-08-372-105-164	Sequence 164, App
54	55	100.0	14	1	US-08-306-473A-164	Sequence 164, App
55	55	100.0	14	1	US-08-261-660A-37	Sequence 37, Appl
56	55	100.0	14	1	US-08-218-026-9	Sequence 9, Appl
57	55	100.0	14	1	US-08-218-026-27	Sequence 27, Appl
58	55	100.0	14	2	US-08-653-632-9	Sequence 9, Appl
59	55	100.0	14	2	US-08-653-632-27	Sequence 27, Appl
60	55	100.0	14	2	US-08-621-803-123	Sequence 123, App
61	55	100.0	14	2	US-08-485-445A-164	Sequence 164, App
62	55	100.0	14	3	US-09-119-263-164	Sequence 164, App
63	55	100.0	14	3	US-08-657-162-164	Sequence 164, App
64	55	100.0	14	3	US-09-224-480-164	Sequence 164, App
65	55	100.0	14	3	US-09-217-352-123	Sequence 123, App
66	55	100.0	14	3	US-09-280-909A-37	Sequence 37, Appl
67	55	100.0	14	3	US-08-477-778-12	Sequence 12, Appl
68	55	100.0	14	4	US-09-689-097-161	Sequence 161, App
69	55	100.0	14	5	PCT-US94-06931-37	Sequence 37, Appl
70	55	100.0	14	5	PCT-US95-00498-164	Sequence 164, App
71	55	100.0	14	5	PCT-US95-00656-164	Sequence 164, App
72	55	100.0	15	1	US-08-311-611A-7	Sequence 7, Appl
73	55	100.0	15	1	US-08-311-611A-16	Sequence 16, Appl
74	55	100.0	15	1	US-08-311-611A-17	Sequence 17, Appl
75	55	100.0	15	1	US-08-311-611A-18	Sequence 18, Appl
76	55	100.0	15	1	US-08-311-611A-19	Sequence 19, Appl
77	55	100.0	15	1	US-08-311-611A-20	Sequence 20, Appl
78	55	100.0	15	1	US-08-311-611A-49	Sequence 49, Appl
79	55	100.0	15	1	US-08-311-611A-51	Sequence 51, Appl
80	55	100.0	15	1	US-08-372-783-7	Sequence 7, Appl
81	55	100.0	15	1	US-08-372-783-16	Sequence 16, Appl
82	55	100.0	15	1	US-08-372-783-17	Sequence 17, Appl
83	55	100.0	15	1	US-08-372-783-18	Sequence 18, Appl
84	55	100.0	15	1	US-08-372-783-19	Sequence 19, Appl
85	55	100.0	15	1	US-08-372-783-20	Sequence 20, Appl
86	55	100.0	15	1	US-08-372-783-49	Sequence 49, Appl
87	55	100.0	15	1	US-08-372-783-51	Sequence 51, Appl
88	55	100.0	15	1	US-08-372-105-7	Sequence 7, Appl
89	55	100.0	15	1	US-08-372-105-16	Sequence 16, Appl
90	55	100.0	15	1	US-08-372-105-17	Sequence 17, Appl
91	55	100.0	15	1	US-08-372-105-18	Sequence 18, Appl
92	55	100.0	15	1	US-08-372-105-19	Sequence 19, Appl
93	55	100.0	15	1	US-08-372-105-20	Sequence 20, Appl
94	55	100.0	15	1	US-08-372-105-49	Sequence 49, Appl
95	55	100.0	15	1	US-08-372-105-51	Sequence 51, Appl
96	55	100.0	15	1	US-08-306-473A-7	Sequence 7, Appl
97	55	100.0	15	1	US-08-306-473A-16	Sequence 16, Appl
98	55	100.0	15	1	US-08-306-473A-17	Sequence 17, Appl
99	55	100.0	15	1	US-08-306-473A-18	Sequence 18, Appl
100	55	100.0	15	1	US-08-306-473A-19	Sequence 19, Appl

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OM protein - protein search, using bw model

Run on: March 26, 2005, 12:17:20 ; Search time 43.6021 Seconds
(without alignments)
75.937 Million cell updates/sec

Title: US-09-124-280A-43
Perfect score: 62
Sequence: 1 CKRFRKFKFC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubppaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubppaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
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- 14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubppaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubppaa/US10D_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	100.0	10	9 US-09-124-280A-43	Sequence 43, Appl1
2	44	71.0	10	9 US-09-124-280A-5	Sequence 5, Appl1
3	41	66.1	584	15 US-10-282-122A-59562	Sequence 59562, A
4	41	66.1	586	15 US-10-282-122A-56612	Sequence 56612, A
5	41	66.1	586	15 US-10-282-122A-74860	Sequence 74860, A
6	41	66.1	586	15 US-10-282-122A-76970	Sequence 76270, A
7	41	66.1	588	15 US-10-282-122A-55937	Sequence 55937, A
8	41	66.1	589	15 US-10-282-122A-68550	Sequence 68550, A
9	39	62.9	178	15 US-10-424-599-231286	Sequence 231286, A
10	39	62.9	585	15 US-10-282-122A-77784	Sequence 77784, A
11	38	61.3	36	14 US-10-029-386-31853	Sequence 31853, A
12	38	61.3	68	15 US-10-424-599-173645	Sequence 173645, A
13	37	59.7	72	15 US-10-424-599-143878	Sequence 143878, A

14	37	59.7	72	15	US-10-425-114-54359	Sequence 54359, A
15	37	59.7	82	15	US-10-425-114-61915	Sequence 61915, A
16	37	59.7	167	15	US-10-437-967-167479	Sequence 167479, A
17	37	59.7	191	15	US-10-335-967-5818	Sequence 5818, A
18	37	59.7	194	10	US-09-882-227-426	Sequence 426, App
19	37	59.7	241	15	US-10-282-122A-52491	Sequence 52491, A
20	37	59.7	447	15	US-10-425-114-55954	Sequence 55954, A
21	37	59.7	663	14	US-10-115-223-30	Sequence 30, Appl1
22	37	59.7	663	15	US-10-402-212-30	Sequence 6, Appl1
23	37	59.7	1120	15	US-10-467-042-6	Sequence 15, Appl1
24	36	58.1	10	9	US-09-124-280A-15	Sequence 15, Appl1
25	36	58.1	12	14	US-10-192-832-15	Sequence 14, Appl1
26	36	58.1	16	9	US-09-778-200-14	Sequence 14, Appl1
27	36	58.1	16	14	US-10-192-832-14	Sequence 14, Appl1
28	36	58.1	69	15	US-10-424-599-230074	Sequence 230074, A
29	36	58.1	85	15	US-10-437-963-155984	Sequence 155984, A
30	36	58.1	93	16	US-10-437-963-118223	Sequence 118223, A
31	36	58.1	169	16	US-10-437-963-125771	Sequence 125771, A
32	36	58.1	364	9	US-09-864-761-33528	Sequence 33528, A
33	36	58.1	467	14	US-10-032-585-723	Sequence 7233, Ap
34	35.5	57.3	61	16	US-10-437-963-191952	Sequence 191952, A
35	35	56.5	60	15	US-10-424-599-184026	Sequence 184026, A
36	35	56.5	70	16	US-10-437-963-193812	Sequence 193812, A
37	35	56.5	97	15	US-10-424-599-268226	Sequence 268226, A
38	35	56.5	107	15	US-10-424-599-202987	Sequence 202987, A
39	35	56.5	146	16	US-10-437-963-184974	Sequence 184974, A
40	35	56.5	238	9	US-09-864-761-33527	Sequence 33527, A
41	35	56.5	276	15	US-10-283-122A-53264	Sequence 53264, A
42	35	56.5	322	16	US-10-437-963-177451	Sequence 177451, A
43	35	56.5	392	9	US-09-989-722-205	Sequence 205, App
44	35	56.5	392	9	US-09-989-722-205	Sequence 205, App
45	35	56.5	392	9	US-09-989-279-205	Sequence 205, App
46	35	56.5	392	9	US-09-989-727-205	Sequence 205, App
47	35	56.5	392	9	US-09-989-731-205	Sequence 205, App
48	35	56.5	392	9	US-09-989-732-205	Sequence 205, App
49	35	56.5	392	9	US-09-991-073-205	Sequence 205, App
50	35	56.5	392	9	US-09-990-442-205	Sequence 205, App
51	35	56.5	392	9	US-09-991-163-205	Sequence 205, App
52	35	56.5	392	9	US-09-993-604-205	Sequence 205, App
53	35	56.5	392	9	US-09-990-456-205	Sequence 205, App
54	35	56.5	392	9	US-09-989-721-205	Sequence 205, App
55	35	56.5	392	9	US-09-992-598-205	Sequence 205, App
56	35	56.5	392	9	US-09-989-293A-205	Sequence 205, App
57	35	56.5	392	9	US-09-989-735-205	Sequence 205, App
58	35	56.5	392	9	US-09-990-444-205	Sequence 205, App
59	35	56.5	392	9	US-09-991-181-205	Sequence 205, App
60	35	56.5	392	9	US-09-989-730-205	Sequence 205, App
61	35	56.5	392	9	US-09-990-436-205	Sequence 205, App
62	35	56.5	392	9	US-09-993-687-205	Sequence 205, App
63	35	56.5	392	10	US-09-989-734-205	Sequence 205, App
64	35	56.5	392	10	US-09-997-653-205	Sequence 205, App
65	35	56.5	392	10	US-09-989-724-205	Sequence 205, App
66	35	56.5	392	10	US-09-989-728-205	Sequence 205, App
67	35	56.5	392	10	US-09-990-441-205	Sequence 205, App
68	35	56.5	392	10	US-09-990-441-205	Sequence 205, App
69	35	56.5	392	10	US-09-993-667-205	Sequence 205, App
70	35	56.5	392	10	US-09-997-428-205	Sequence 205, App
71	35	56.5	392	10	US-09-997-666-205	Sequence 205, App
72	35	56.5	392	10	US-09-991-157-205	Sequence 205, App
73	35	56.5	392	10	US-09-997-514-205	Sequence 205, App
74	35	56.5	392	10	US-09-997-711-205	Sequence 205, App
75	35	56.5	392	10	US-09-990-711-205	Sequence 205, App
76	35	56.5	392	10	US-09-989-726-205	Sequence 205, App
77	35	56.5	392	10	US-09-990-437-205	Sequence 205, App
78	35	56.5	392	10	US-09-991-157-205	Sequence 205, App
79	35	56.5	392	10	US-09-997-514-205	Sequence 205, App
80	35	56.5	392	10	US-09-997-711-205	Sequence 205, App
81	35	56.5	392	10	US-09-991-112-205	Sequence 205, App
82	35	56.5	392	10	US-09-990-726-205	Sequence 205, App
83	35	56.5	392	10	US-09-997-559-205	Sequence 205, App
84	35	56.5	392	10	US-09-997-601-205	Sequence 205, App
85	35	56.5	392	10	US-09-990-443-205	Sequence 205, App
86	35	56.5	392	10	US-09-991-854-205	Sequence 205, App

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OM protein - protein search, using SW model

Run on: March 26, 2005, 10:54:27 ; Search time 17.043 Seconds
(without alignments)
43.800 Million cell updates/sec

Title: US-09-124-280A-43
Perfect score: 1
Sequence: 1 CKEFKFKFC 10

Scoring table: BLAST62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database: Issued Patents AA:
1: /cgn2_6/prodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/prodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/prodata/1/1aa/5C.COMB.pep.*
4: /cgn2_6/prodata/1/1aa/5D.COMB.pep.*
5: /cgn2_6/prodata/1/1aa/5E.COMB.pep.*
6: /cgn2_6/prodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	62	100.0	10	2	US-08-456-112B-43
2	44	71.0	10	1	US-08-097-830E-5
3	44	71.0	10	2	US-08-456-112B-5
4	44	71.0	51	4	US-09-270-767-37773
5	44	71.0	51	4	US-09-270-767-52990
6	41	66.1	589	4	US-09-489-039A-8395
7	41	66.1	590	4	US-09-543-681A-7931
8	39	62.9	152	4	US-09-270-767-38287
9	39	62.9	152	4	US-09-270-767-53504
10	39	62.9	359	4	US-09-270-767-61061
11	39	62.9	475	4	US-09-270-767-45548
12	38	61.3	150	4	US-09-270-767-46076
13	37	59.7	137	4	US-09-270-767-44232
14	37	59.7	137	4	US-09-270-767-49439
15	37	59.7	184	4	US-09-270-767-35284
16	37	59.7	184	4	US-09-270-767-35284
17	37	59.7	663	4	US-09-270-767-50501
18	36	58.1	10	1	US-08-194-468A-30
19	36	58.1	10	2	US-08-097-830E-15
20	36	58.1	72	4	US-08-456-112B-15
21	36	58.1	72	4	US-08-583-110-4345
22	36	58.1	74	4	US-09-248-796A-22981
23	36	58.1	80	4	US-09-248-796A-26570
24	36	58.1	295	4	US-09-107-433-4711
25	36	58.1	295	4	US-09-270-767-61784
26	36	58.1	314	2	US-08-460-309-19
27	36	58.1	553	4	US-08-125-077-19

28	35	56.5	61	4	US-09-248-796A-24527	Sequence 24527, A
29	35	56.5	64	4	US-09-248-796A-25040	Sequence 25040, A
30	35	56.5	212	4	US-09-270-767-58517	Sequence 58517, A
31	35	56.5	390	4	US-09-270-767-43178	Sequence 43178, A
32	35	56.5	393	4	US-09-482-273-154	Sequence 154, App
33	35	56.5	407	3	US-09-399-913-53	Sequence 53, Appl
34	35	56.5	407	3	US-09-350-614-55	Sequence 53, Appl
35	35	56.5	414	3	US-09-399-913-55	Sequence 55, Appl
36	35	56.5	414	3	US-09-350-614-55	Sequence 55, Appl
37	34	54.8	92	4	US-09-270-767-58304	Sequence 58304, A
38	34	54.8	216	4	US-09-328-352-7215	Sequence 7215, Ap
39	34	54.8	292	4	US-09-270-767-43169	Sequence 43169, A
40	34	54.8	402	4	US-09-540-236-2685	Sequence 2685, Ap
41	34	54.8	429	4	US-09-194-468A-45	Sequence 45, Appl
42	34	54.8	435	4	US-09-270-767-42976	Sequence 42976, A
43	34	54.8	441	4	US-09-949-016-10792	Sequence 10792, A
44	34	54.8	560	4	US-09-949-016-6458	Sequence 6458, Ap
45	34	54.8	560	4	US-09-912-553-3	Sequence 3, Appl
46	34	54.8	560	4	US-09-912-553-4	Sequence 4, Appl
47	34	54.8	631	3	US-08-448-489-17	Sequence 17, Appl
48	34	54.8	631	3	US-08-689-730-17	Sequence 17, Appl
49	34	54.8	660	3	US-08-704-711A-18	Sequence 18, Appl
50	34	54.8	660	3	US-09-521-220-18	Sequence 18, Appl
51	34	54.8	660	3	US-09-391-104-19	Sequence 19, Appl
52	34	54.8	660	3	US-09-917-254-89	Sequence 89, Appl
53	34	54.8	660	4	US-09-949-016-6512	Sequence 6512, Ap
54	34	54.8	660	4	US-09-949-016-7937	Sequence 7937, Ap
55	34	54.8	754	4	US-09-270-767-45853	Sequence 45853, A
56	33	54.0	331	4	US-09-328-352-5339	Sequence 5339, Ap
57	33	53.2	10	1	US-08-311-611A-165	Sequence 165, App
58	33	53.2	10	1	US-08-372-783-165	Sequence 165, App
59	33	53.2	10	1	US-08-372-105-165	Sequence 165, App
60	33	53.2	10	1	US-08-306-472A-165	Sequence 165, App
61	33	53.2	10	2	US-08-621-803-124	Sequence 124, App
62	33	53.2	10	2	US-08-485-445A-165	Sequence 165, App
63	33	53.2	10	3	US-09-119-263-165	Sequence 165, App
64	33	53.2	10	3	US-08-657-163-165	Sequence 165, App
65	33	53.2	10	3	US-09-224-480-165	Sequence 165, App
66	33	53.2	10	3	US-09-217-352-124	Sequence 124, App
67	33	53.2	10	3	US-08-477-778-13	Sequence 13, Appl
68	33	53.2	10	4	US-09-689-097-162	Sequence 162, App
69	33	53.2	10	5	PCT-US95-00498-165	Sequence 165, App
70	33	53.2	10	5	PCT-US95-00656-165	Sequence 165, App
71	33	53.2	71	4	US-09-134-000C-3597	Sequence 3597, Ap
72	33	53.2	129	4	US-10-000-489-98	Sequence 98, Appl
73	33	53.2	131	4	US-10-000-489-84	Sequence 84, Appl
74	33	53.2	131	4	US-09-270-767-38389	Sequence 38389, A
75	33	53.2	133	4	US-09-270-767-53606	Sequence 53606, A
76	33	53.2	133	4	US-09-228-986-87	Sequence 87, Appl
77	33	53.2	156	3	US-10-101-464A-87	Sequence 87, Appl
78	33	53.2	156	4	US-10-101-464A-87	Sequence 87, Appl
79	33	53.2	157	4	US-10-101-464A-87	Sequence 87, Appl
80	33	53.2	158	4	US-09-270-767-36587	Sequence 36587, A
81	33	53.2	158	4	US-09-270-767-51804	Sequence 51804, A
82	33	53.2	160	4	US-09-248-796A-16629	Sequence 16629, A
83	33	53.2	176	4	US-09-270-767-60073	Sequence 60073, A
84	33	53.2	200	4	US-09-134-000C-3505	Sequence 3505, Ap
85	33	53.2	258	4	US-09-270-767-44625	Sequence 44625, A
86	33	53.2	271	4	US-09-270-767-35990	Sequence 35990, A
87	33	53.2	271	4	US-09-270-767-51207	Sequence 51207, A
88	33	53.2	271	4	US-09-270-767-45401	Sequence 45401, A
89	33	53.2	349	4	US-09-270-767-45401	Sequence 45401, A
90	33	53.2	387	4	US-09-270-767-45451	Sequence 45451, A
91	33	53.2	437	4	US-09-248-796A-19098	Sequence 19098, A
92	33	53.2	437	4	US-09-369-913A-19	Sequence 19, Appl
93	33	53.2	446	2	US-07-728-215-33	Sequence 33, Appl
94	33	53.2	446	2	US-08-938-085A-33	Sequence 33, Appl
95	33	53.2	846	4	US-10-072-844-33	Sequence 33, Appl
96	33	53.2	846	4	US-10-072-844-33	Sequence 33, Appl
97	33	53.2	846	4	US-10-072-844A-33	Sequence 33, Appl
98	33	53.2	846	4	US-10-219-631A-33	Sequence 33, Appl
99	33	53.2	1081	3	US-09-369-364A-17	Sequence 17, Appl
100	32.5	52.4	83	3	US-09-981-953A-4	Sequence 4, Appl

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OM protein - protein search, using sw model

Run on: March 26, 2005, 12:17:20 ; Search time 43.6021 Seconds
(without alignments)

75.937 Million cell updates/sec

Title: US-09-124-280a-42

Perfect score: 50

Sequence: 1 KKKKKKFLFL 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

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2: /cgn2_6/ptodata/1/pubpa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpa/US06_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/1/pubpa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpa/US11_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	10	9	US-09-124-280a-42
2	44	88.0	60	16	US-10-437-963-187972
3	42	84.0	58	16	US-10-437-963-193655
4	42	84.0	67	16	US-10-437-963-192982
5	42	84.0	116	16	US-10-437-963-115875
6	42	84.0	121	16	US-10-437-963-116634
7	41	82.0	53	16	US-10-767-701-51594
8	41	82.0	90	15	US-10-424-599-184179
9	40	80.0	10	9	US-09-124-280a-12
10	40	80.0	54	15	US-10-424-599-258128
11	40	80.0	93	16	US-10-437-963-165310
12	40	80.0	114	15	US-10-424-599-264693
13	40	80.0	221	16	US-10-767-701-51748

14	40	80.0	602	15	US-10-104-047-3092	Sequence 3092, Ap
15	39	78.0	59	16	US-10-437-963-189929	Sequence 189929, Ap
16	39	78.0	62	15	US-10-424-599-161859	Sequence 161859, Ap
17	39	78.0	90	15	US-10-424-599-166534	Sequence 166534, Ap
18	39	78.0	91	16	US-10-437-963-143299	Sequence 143299, Ap
19	39	78.0	92	16	US-10-437-963-202680	Sequence 202680, Ap
20	39	78.0	766	15	US-10-664-456-12	Sequence 12, Appl
21	39	78.0	870	15	US-10-664-456-13	Sequence 13, Appl
22	39	78.0	820	15	US-10-664-456-14	Sequence 14, Appl
23	39	78.0	820	16	US-10-408-765A-1252	Sequence 1252, Ap
24	38	76.0	43	15	US-10-424-599-223572	Sequence 223572, Ap
25	38	76.0	65	15	US-10-424-599-281525	Sequence 281525, Ap
26	38	76.0	68	15	US-10-424-599-242981	Sequence 242981, Ap
27	38	76.0	79	15	US-10-424-599-277607	Sequence 277607, Ap
28	38	76.0	84	15	US-10-424-599-267131	Sequence 267131, Ap
29	38	76.0	98	15	US-10-425-114-41617	Sequence 41617, A
30	38	76.0	99	15	US-10-424-599-172391	Sequence 172391, A
31	38	76.0	99	15	US-10-424-599-256567	Sequence 256567, Ap
32	38	76.0	100	15	US-10-424-599-275312	Sequence 275312, Ap
33	38	76.0	184	10	US-09-862-540-57	Sequence 57, Appl
34	38	76.0	197	16	US-10-437-963-135809	Sequence 135809, Ap
35	37	74.0	15	14	US-10-174-105A-191	Sequence 191, Appl
36	37	74.0	20	10	US-09-380-682-62	Sequence 62, Appl
37	37	74.0	25	9	US-09-999-745-42	Sequence 42, Appl
38	37	74.0	25	9	US-09-554-000-26	Sequence 26, Appl
39	37	74.0	25	17	US-10-857-622-46	Sequence 46, Appl
40	37	74.0	42	15	US-10-424-599-236786	Sequence 236786, Ap
41	37	74.0	43	10	US-09-911-569-89	Sequence 89, Appl
42	37	74.0	43	14	US-10-200-879-89	Sequence 89, Appl
43	37	74.0	46	13	US-10-001-870-181	Sequence 181, Appl
44	37	74.0	47	15	US-10-424-599-255768	Sequence 255768, Ap
45	37	74.0	54	14	US-09-911-569-90	Sequence 90, Appl
46	37	74.0	54	10	US-10-200-879-90	Sequence 90, Appl
47	37	74.0	58	15	US-10-424-599-147944	Sequence 147944, Ap
48	37	74.0	61	15	US-10-424-599-182565	Sequence 182565, Ap
49	37	74.0	71	15	US-10-424-599-272979	Sequence 272979, Ap
50	37	74.0	73	15	US-10-424-599-178675	Sequence 178675, Ap
51	37	74.0	78	16	US-10-437-963-115443	Sequence 115443, Ap
52	37	74.0	80	14	US-10-078-090-181	Sequence 181, Appl
53	37	74.0	104	16	US-10-437-963-127614	Sequence 127614, Ap
54	37	74.0	112	15	US-10-424-599-201313	Sequence 201313, Ap
55	37	74.0	129	15	US-10-424-599-186256	Sequence 186256, Ap
56	37	74.0	129	15	US-10-424-599-253461	Sequence 253461, Ap
57	37	74.0	146	15	US-10-424-599-285071	Sequence 285071, Ap
58	37	74.0	156	15	US-10-424-599-221095	Sequence 221095, Ap
59	37	74.0	200	15	US-10-424-599-218629	Sequence 218629, Ap
60	37	74.0	243	16	US-10-437-963-177145	Sequence 177145, Ap
61	37	74.0	266	14	US-10-032-585-7055	Sequence 7055, Ap
62	37	74.0	389	15	US-10-131-410-172	Sequence 172, Appl
63	37	74.0	601	16	US-10-437-963-122724	Sequence 122724, Ap
64	36	72.0	35	13	US-10-001-857-134	Sequence 134, Appl
65	36	72.0	36	10	US-09-911-569-91	Sequence 91, Appl
66	36	72.0	36	14	US-10-200-879-91	Sequence 91, Appl
67	36	72.0	40	15	US-10-424-599-238827	Sequence 238827, Ap
68	36	72.0	41	10	US-09-764-891-2768	Sequence 2768, Ap
69	36	72.0	41	14	US-10-205-428-259	Sequence 259, Appl
70	36	72.0	43	15	US-10-424-599-246379	Sequence 246379, Ap
71	36	72.0	44	14	US-09-911-569-88	Sequence 88, Appl
72	36	72.0	44	14	US-10-200-879-88	Sequence 88, Appl
73	36	72.0	46	16	US-10-437-963-127920	Sequence 127920, Ap
74	36	72.0	47	15	US-10-424-599-285054	Sequence 285054, Ap
75	36	72.0	48	15	US-10-424-599-248487	Sequence 248487, Ap
76	36	72.0	49	15	US-10-424-599-177679	Sequence 177679, Ap
77	36	72.0	50	15	US-10-424-599-193863	Sequence 193863, Ap
78	36	72.0	50	15	US-10-424-599-202419	Sequence 202419, Ap
79	36	72.0	50	15	US-10-424-599-239261	Sequence 239261, Ap
80	36	72.0	52	15	US-10-424-599-143227	Sequence 143227, Ap
81	36	72.0	53	15	US-10-437-963-158929	Sequence 158929, Ap
82	36	72.0	53	16	US-10-424-599-161700	Sequence 161700, Ap
83	36	72.0	56	14	US-10-106-698-9569	Sequence 9569, Ap
84	36	72.0	56	15	US-10-424-599-165415	Sequence 165415, Ap
85	36	72.0	56	16	US-10-767-701-51073	Sequence 51073, A
86	36	72.0	58	15	US-10-424-599-168696	Sequence 168696, A

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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:54:27 ; Search time 17.043 Seconds
(without alignments)
43,800 Million cell updates/sec

Title: US-09-124-280A-42
Perfect score: 50
Sequence: 1 KKKKKKFLPL 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database: Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.rep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.rep:*
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- 5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.rep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.rep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	50	100.0	10 2 US-08-456-1128-42	Sequence 42, Appl
2	41	82.0	29 3 US-09-093-327-30	Sequence 30, Appl
3	41	82.0	30 3 US-09-093-327-31	Sequence 31, Appl
4	41	82.0	68 4 US-09-248-796A-25135	Sequence 25135, A
5	41	82.0	419 4 US-09-270-767-46795	Sequence 46795, A
6	40	80.0	10 1 US-08-097-830E-12	Sequence 12, Appl
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March 26, 2005, 12:17:20 / Search time 43.6021 Seconds

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US-09-124-280a-41

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67	31	63.3	207 3	US-09-134-001C-4726	Sequence 4726, Ap
68	31	63.3	233 4	US-09-270-767-45076	Sequence 45076, A
69	31	63.3	242 4	US-09-198-452A-182	Sequence 182, App
70	31	63.3	316 4	US-09-538-092-772	Sequence 772, App
71	31	63.3	341 4	US-09-248-796A-15858	Sequence 15858, A
72	31	63.3	356 4	US-09-438-185A-164	Sequence 164, App
73	31	63.3	400 4	US-09-198-452A-202	Sequence 202, App
74	31	63.3	400 4	US-09-438-185A-291	Sequence 291, App
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78	31	63.3	2254 2	US-08-286-819A-28	Sequence 28, Appl
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83	30	61.2	103 4	US-09-732-210-1231	Sequence 1231, Ap
84	30	61.2	114 4	US-09-540-236-1379	Sequence 1379, Ap
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94	30	61.2	185 3	US-09-092-179-2	Sequence 2, Appl
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OM protein - protein search, using sw model

Run on: March 26, 2005, 12:17:20 / Search time 39.2419 Seconds
(without alignments)
75.937 Million cell updates/sec

Title: US-09-124-280A-40
Perfect score: 51
Sequence: 1 KFFKFFKFF 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1407402 seqs, 33110923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database:

Published Applications AA:
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2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	51	100.0	9 15 US-10-240-641-8	Sequence 8, Appl
5	51	100.0	10 9 US-09-124-280A-10	Sequence 10, Appl
6	51	100.0	10 14 US-10-083-259-148	Sequence 148, Appl
7	51	100.0	10 14 US-10-109-274A-148	Sequence 148, Appl
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17	45	88.2	8 15 US-10-240-641-9	Sequence 9, Appl
18	45	88.2	9 14 US-10-083-259-151	Sequence 151, Appl
19	45	88.2	9 14 US-10-083-259-152	Sequence 152, Appl
20	45	88.2	9 14 US-10-109-274A-151	Sequence 151, Appl
21	45	88.2	9 14 US-10-109-274A-152	Sequence 152, Appl
22	40	78.4	9 14 US-10-083-259-6	Sequence 6, Appl
23	40	78.4	9 14 US-10-109-274A-6	Sequence 6, Appl
24	40	78.4	9 15 US-10-240-641-14	Sequence 14, Appl
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28	39	76.5	7 15 US-10-109-274A-157	Sequence 10, Appl
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31	38	74.5	36 15 US-10-424-599-240811	Sequence 11505, Sequence 171741
32	38	74.5	43 15 US-10-424-599-198109	Sequence 225194, Sequence 144396
33	38	74.5	59 16 US-10-437-963-189937	Sequence 247110, Sequence 198742
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38	37	72.5	106 15 US-10-424-599-144396	Sequence 80, Appl
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43	36	70.6	69 15 US-10-424-599-197518	Sequence 374, Appl
44	36	70.6	71 15 US-10-424-599-145989	Sequence 65, Appl
45	36	70.6	71 16 US-10-437-963-166186	Sequence 58, Appl
46	36	70.6	117 16 US-10-437-963-169083	Sequence 252226, Sequence 193526
47	36	70.6	233 16 US-10-437-963-166971	Sequence 1020, Appl
48	36	70.6	352 16 US-10-369-493-15522	Sequence 269130, Sequence 204505
49	36	70.6	332 16 US-10-451-467A-80	Sequence 103260, Sequence 102260
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51	36	70.6	414 9 US-09-932-474-1	Sequence 170739, Sequence 88, Appl
52	36	70.6	414 17 US-10-278-946-2	Sequence 115122, Sequence 154286
53	36	70.6	414 14 US-10-967-189-2	Sequence 154286, Sequence 189937
54	36	70.6	698 15 US-10-369-493-22791	Sequence 189937, Sequence 153280
55	36	70.6	875 15 US-10-376-774-1761	Sequence 167174, Sequence 167174
56	36	70.6	881 16 US-10-322-261-374	Sequence 7981, Appl
57	35	68.6	18 10 US-09-747-802-55	Sequence 2565, Appl
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61	35	68.6	46 15 US-10-424-599-153226	
62	35	68.6	54 15 US-10-424-599-193526	
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On protein - protein search, using sw model

Run: March 26, 2005, 10:54:27 ; Search time 15.3387 Seconds
(without alignments)

43.800 Million cell updates/sec

Title: US-09-124-280A-40

Perfect score: 51

Sequence: 1 KPFFKFFKFP 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database: Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	38	74.5	313	4	US-09-270-767-58683
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8	37	72.5	77	4	US-09-328-352-7597
9	36	70.6	67	4	US-09-270-767-35751
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11	36	70.6	118	4	US-09-248-796A-28195
12	36	70.6	401	4	US-09-489-039A-8992
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OM protein - protein search, using sw model

Run on: March 26, 2005, 12:17:20 ; Search time 39.2419 Seconds
(without alignments)
75.937 Million cell updates/sec

Title: US-09-124-280A-39
Perfect score: 48
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Gapop 10.0, Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	9	US-09-124-280A-9	Sequence 9, Appli
2	48	100.0	9	US-09-124-280A-39	Sequence 39, Appli
3	43	89.6	1460	US-10-437-963-142150	Sequence 142150,
4	36	75.0	381	US-10-156-761-9518	Sequence 9518, Ap
5	35	72.9	87	US-10-437-963-139862	Sequence 139862,
6	35	72.9	101	US-09-738-626-5727	Sequence 5727, Ap
7	35	72.9	122	US-09-095-478-4	Sequence 4, Appli
8	35	72.9	122	US-09-095-478-5	Sequence 5, Appli
9	35	72.9	225	US-10-437-963-139861	Sequence 139861,
10	35	72.9	320	US-10-369-493-370	Sequence 370, App
11	35	72.9	335	US-10-369-493-12122	Sequence 2122, A
12	35	72.9	354	US-09-095-478-6	Sequence 6, Appli
13	35	72.9	379	US-09-095-478-8	Sequence 8, Appli

14	35	72.9	412	US-09-095-478-3	Sequence 3, Appli
15	35	72.9	426	US-09-095-478-1	Sequence 1, Appli
16	35	72.9	463	US-09-095-478-2	Sequence 2, Appli
17	35	72.9	1802	US-10-437-963-139865	Sequence 139865,
18	34	70.8	36	US-10-351-641-605	Sequence 605, App
19	34	70.8	36	US-10-351-641-606	Sequence 606, App
20	34	70.8	36	US-10-351-641-607	Sequence 607, App
21	34	70.8	49	US-09-764-864-1054	Sequence 1054, Ap
22	34	70.8	52	US-10-106-664-5631	Sequence 5631, Ap
23	34	70.8	83	US-09-764-877-1607	Sequence 1607, Ap
24	34	70.8	83	US-10-242-515-1607	Sequence 1607, Ap
25	34	70.8	83	US-10-424-599-185970	Sequence 185970,
26	34	70.8	108	US-10-424-599-275790	Sequence 275790,
27	34	70.8	116	US-10-424-599-198592	Sequence 198592,
28	34	70.8	168	US-10-767-701-51428	Sequence 51428, A
29	34	70.8	255	US-10-380-254-2	Sequence 2, Appli
30	34	70.8	334	US-10-282-122A-68938	Sequence 68938, A
31	34	70.8	361	US-10-274-694-11	Sequence 11, Appli
32	34	70.8	362	US-10-104-047-3160	Sequence 3160, Ap
33	34	70.8	438	US-09-908-419-2	Sequence 2, Appli
34	34	70.8	438	US-10-056-790-36	Sequence 36, Appli
35	34	70.8	438	US-10-056-790-36	Sequence 36, Appli
36	34	70.8	470	US-10-056-790-46	Sequence 46, Appli
37	34	70.8	600	US-09-601-368-158	Sequence 158, App
38	34	70.8	947	US-10-437-963-114679	Sequence 114679,
39	34	70.8	2172	US-10-437-963-195816	Sequence 195816,
40	33	68.8	74	US-10-425-114-65765	Sequence 65765, A
41	33	68.8	235	US-10-437-963-202951	Sequence 202951,
42	33	68.8	235	US-10-437-963-202951	Sequence 202951,
43	33	68.8	350	US-10-437-963-118034	Sequence 118034,
44	33	68.8	350	US-10-437-963-118034	Sequence 118034,
45	33	68.8	376	US-10-425-114-54205	Sequence 54205, A
46	33	68.8	388	US-10-767-701-40025	Sequence 40025, A
47	33	68.8	421	US-10-769-762-932	Sequence 932, App
48	33	68.8	630	US-10-128-714-8935	Sequence 8935, App
49	33	68.8	665	US-10-437-963-117047	Sequence 117047,
50	33	68.8	705	US-10-425-114-65776	Sequence 65776, A
51	33	68.8	832	US-10-267-502-303	Sequence 303, App
52	33	68.8	1095	US-10-369-493-20225	Sequence 2025, App
53	33	68.8	1160	US-10-115-641-608	Sequence 608, App
54	32	66.7	36	US-10-351-641-609	Sequence 609, App
55	32	66.7	86	US-10-437-963-140300	Sequence 140300,
56	32	66.7	222	US-10-424-599-284866	Sequence 284866,
57	32	66.7	306	US-10-369-493-22664	Sequence 22664, A
58	32	66.7	432	US-10-369-493-12020	Sequence 12020, A
59	32	66.7	463	US-10-437-963-144541	Sequence 144541,
60	32	66.7	536	US-10-437-963-157400	Sequence 157400,
61	32	66.7	638	US-10-072-621-10	Sequence 10, Appli
62	32	66.7	666	US-10-267-502-309	Sequence 309, App
63	32	66.7	674	US-10-090-455-4	Sequence 4, Appli
64	32	66.7	674	US-10-429-160-10	Sequence 10, Appli
65	32	66.7	674	US-10-267-502-307	Sequence 307, App
66	32	66.7	674	US-10-648-593-214	Sequence 214, App
67	32	66.7	778	US-10-437-963-157402	Sequence 157402,
68	32	66.7	803	US-10-320-797-3298	Sequence 3298, App
69	32	66.7	861	US-10-441-926-20	Sequence 20, Appli
70	32	66.7	861	US-10-441-926-22	Sequence 22, Appli
71	32	66.7	861	US-10-441-926-24	Sequence 24, Appli
72	32	66.7	861	US-10-441-926-26	Sequence 26, Appli
73	32	66.7	861	US-10-441-926-28	Sequence 28, Appli
74	32	66.7	861	US-10-441-926-30	Sequence 30, Appli
75	32	66.7	892	US-10-369-493-22811	Sequence 22811, A
76	31	64.6	9	US-10-424-599-204620	Sequence 204620,
77	31	64.6	56	US-10-424-599-230354	Sequence 230354,
78	31	64.6	58	US-10-424-599-230354	Sequence 230354,
79	31	64.6	98	US-10-437-963-182666	Sequence 182666,
80	31	64.6	105	US-09-925-299-1017	Sequence 1017, App
81	31	64.6	105	US-10-424-599-168085	Sequence 168085,
82	31	64.6	126	US-10-424-599-191438	Sequence 191438,
83	31	64.6	170	US-10-424-599-191438	Sequence 191438,
84	31	64.6	228	US-10-282-122A-69949	Sequence 69949, A
85	31	64.6	250	US-09-813-453A-3	Sequence 3, Appli
86	31	64.6	304	US-10-320-797-3113	Sequence 3113, App

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OM protein - protein search, using ew model

Run on: March 26, 2005, 10:54:27 ; Search time 15.3387 Seconds

(without alignments)
43.800 Million cell updates/sec

Title: US-09-124-280A-39

Perfect score: 48

Sequence: 1 RYRYRYRY 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	9	1	US-07-819-893-10
2	48	100.0	9	1	US-08-280-397-10
3	48	100.0	9	1	US-08-097-830E-9
4	48	100.0	9	2	US-08-456-112B-9
5	48	100.0	9	2	US-08-456-112B-9
6	35	72.9	110	4	US-09-732-210-457
7	34	70.8	36	3	US-09-082-279B-605
8	34	70.8	36	3	US-09-082-279B-605
9	34	70.8	36	3	US-09-082-279B-605
10	34	70.8	36	3	US-09-315-304B-605
11	34	70.8	36	3	US-09-315-304B-605
12	34	70.8	36	3	US-09-315-304B-605
13	34	70.8	36	3	US-09-315-304B-605
14	34	70.8	36	3	US-09-834-784-605
15	34	70.8	36	3	US-09-834-784-605
16	34	70.8	36	3	US-09-834-784-605
17	34	70.8	36	3	US-09-834-784-605
18	34	70.8	36	3	US-09-515-965A-605
19	34	70.8	36	3	US-09-515-965A-605
20	34	70.8	36	3	US-09-515-965A-605
21	34	70.8	36	3	US-09-515-965A-605
22	34	70.8	36	3	US-09-350-641C-605
23	34	70.8	36	3	US-09-350-641C-605
24	34	70.8	36	3	US-09-350-641C-605
25	34	70.8	36	3	US-09-350-641C-605
26	34	70.8	36	3	US-09-350-641C-605
27	34	70.8	36	3	US-09-350-641C-605

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OM protein - protein search, using sw model

Run on: March 26, 2005, 12:17:20 ; Search time 30.5215 Seconds

(without alignment)
75.937 Million cell updates/sec

Title: US-09-124-280A-38

Perfect score: 35

Sequence: 1 KFLKFLK 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA:*

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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/FCI_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09D_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US10G_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US10H_PUBCOMB.pep.*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
31	100.0	7	9	US-09-124-280A-7	Sequence 7, Appl
32	100.0	7	9	US-09-124-280A-8	Sequence 38, Appl
33	100.0	10	9	US-09-124-280A-8	Sequence 8, Appl
34	100.0	10	9	US-09-124-280A-41	Sequence 41, Appl
35	100.0	11	9	US-09-124-280A-37	Sequence 37, Appl
36	100.0	12	9	US-09-124-280A-20	Sequence 20, Appl
37	100.0	209	16	US-10-437-963-147868	Sequence 147868
38	100.0	476	15	US-10-282-122A-53100	Sequence 53100, A
39	91.4	66	15	US-10-424-599-152246	Sequence 152246
40	91.4	116	15	US-10-424-599-251225	Sequence 251225
41	91.4	1001	15	US-10-607-631-10	Sequence 10, Appl
42	88.6	9	15	US-10-247-476B-13	Sequence 13, Appl
43	88.6	9	15	US-10-247-476B-14	Sequence 14, Appl

14	31	88.6	61	15	US-10-424-599-212895	Sequence 212895
15	31	88.6	785	16	US-10-437-963-133586	Sequence 133586
16	31	88.6	1012	16	US-10-437-963-170591	Sequence 170591
17	30	85.7	42	15	US-10-424-599-284782	Sequence 284782
18	30	85.7	45	14	US-10-029-386-29370	Sequence 29370, A
19	30	85.7	45	15	US-10-424-599-221561	Sequence 221561
20	30	85.7	65	15	US-10-424-599-203343	Sequence 203343
21	30	85.7	77	15	US-10-424-599-198418	Sequence 198418
22	30	85.7	114	16	US-10-767-701-56234	Sequence 56234, A
23	30	85.7	208	15	US-10-282-122A-45253	Sequence 45253, A
24	30	85.7	212	10	US-09-791-932-84	Sequence 84, Appl
25	30	85.7	228	15	US-10-425-114-70797	Sequence 70797, A
26	30	85.7	229	16	US-10-437-963-166745	Sequence 166745
27	30	85.7	230	16	US-10-437-963-104213	Sequence 104213
28	30	85.7	251	15	US-10-110-154-707	Sequence 707, Appl
29	30	85.7	289	13	US-10-047-676A-4	Sequence 4, Appl
30	30	85.7	309	9	US-09-801-368-290	Sequence 290, Appl
31	30	85.7	577	16	US-10-631-581-31	Sequence 31, Appl
32	30	85.7	670	14	US-10-032-585-7568	Sequence 7568, Ap
33	30	85.7	679	15	US-10-282-122A-52428	Sequence 52428, A
34	30	85.7	957	16	US-10-437-963-167447	Sequence 167447
35	30	85.7	967	15	US-10-425-114-58755	Sequence 58755, A
36	30	85.7	967	15	US-10-425-114-62853	Sequence 62853, A
37	30	85.7	1171	15	US-10-282-122A-51805	Sequence 51805, A
38	29	82.9	18	16	US-10-302-547-124	Sequence 124, Appl
39	29	82.9	74	15	US-10-424-599-243043	Sequence 243043
40	29	82.9	75	15	US-10-424-599-159533	Sequence 159533
41	29	82.9	99	15	US-10-424-599-269978	Sequence 269978
42	29	82.9	181	16	US-10-767-701-37460	Sequence 37460, A
43	29	82.9	205	15	US-10-424-599-212824	Sequence 212824
44	29	82.9	248	15	US-10-424-599-265470	Sequence 265470
45	29	82.9	249	16	US-10-437-963-132560	Sequence 132560
46	29	82.9	262	16	US-10-437-963-132559	Sequence 132559
47	29	82.9	306	15	US-10-425-114-66492	Sequence 66492, A
48	29	82.9	346	15	US-10-425-114-56348	Sequence 56348, A
49	29	82.9	360	15	US-10-425-114-65994	Sequence 65994, A
50	29	82.9	461	16	US-10-767-701-44395	Sequence 44395, A
51	29	82.9	485	15	US-10-369-493-4906	Sequence 4906, Ap
52	29	82.9	536	15	US-10-369-493-7664	Sequence 7664, Ap
53	29	82.9	564	15	US-10-369-493-1706	Sequence 1706, Ap
54	29	82.9	564	15	US-10-369-493-2006	Sequence 2006, Ap
55	29	82.9	987	16	US-10-437-963-118932	Sequence 118932
56	29	82.9	1014	15	US-10-424-599-157075	Sequence 157075
57	29	82.9	1279	10	US-09-882-227-388	Sequence 388, App
58	29	82.9	2223	15	US-10-628-088-408	Sequence 408, App
59	28	80.0	43	15	US-10-424-599-285041	Sequence 285041
60	28	80.0	50	9	US-09-864-761-38298	Sequence 38298, A
61	28	80.0	63	15	US-10-424-599-155562	Sequence 155562
62	28	80.0	67	15	US-10-221-172-312	Sequence 312, App
63	28	80.0	67	15	US-10-221-276-312	Sequence 276, App
64	28	80.0	72	15	US-10-424-599-213192	Sequence 213192
65	28	80.0	73	15	US-10-264-049-2302	Sequence 2302, Ap
66	28	80.0	83	15	US-10-424-599-266486	Sequence 266486
67	28	80.0	102	15	US-10-424-599-269104	Sequence 269104
68	28	80.0	106	15	US-10-291-172-688	Sequence 688, App
69	28	80.0	106	15	US-10-221-276-688	Sequence 688, App
70	28	80.0	112	15	US-10-424-599-15874	Sequence 15874
71	28	80.0	115	15	US-10-425-114-68048	Sequence 68048, A
72	28	80.0	250	14	US-10-234-432-25	Sequence 25, Appl
73	28	80.0	257	10	US-09-870-406A-53	Sequence 53, Appl
74	28	80.0	277	14	US-10-159-901-53	Sequence 53, Appl
75	28	80.0	299	14	US-10-042-894A-10	Sequence 10, Appl
76	28	80.0	299	15	US-10-424-599-249309	Sequence 249309
77	28	80.0	288	15	US-10-264-237-24568	Sequence 24568, Ap
78	28	80.0	321	9	US-09-889-723-36	Sequence 36, Appl
79	28	80.0	321	9	US-09-889-723-36	Sequence 36, Appl
80	28	80.0	321	9	US-09-889-723-36	Sequence 36, Appl
81	28	80.0	321	9	US-09-889-723-36	Sequence 36, Appl
82	28	80.0	321	9	US-09-889-723-36	Sequence 36, Appl
83	28	80.0	321	9	US-09-889-723-36	Sequence 36, Appl
84	28	80.0	321	9	US-09-889-723-36	Sequence 36, Appl
85	28	80.0	321	9	US-09-889-723-36	Sequence 36, Appl
86	28	80.0	321	9	US-09-889-723-36	Sequence 36, Appl

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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:54:27 ; Search time 11.9301 Seconds
(Without alignments)
43.800 Million cell updates/sec

Title: US-09-124-280a-38

Perfect score: 35 KLFKFLK 7

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	7	1 US-07-819-893-9	Sequence 9, Appl1
2	35	100.0	7	1 US-08-280-397-9	Sequence 7, Appl1
3	35	100.0	7	1 US-08-097-830E-7	Sequence 7, Appl1
4	35	100.0	7	2 US-08-456-112B-7	Sequence 7, Appl1
5	35	100.0	7	2 US-08-456-112B-38	Sequence 8, Appl1
6	35	100.0	10	1 US-08-097-830E-8	Sequence 8, Appl1
7	35	100.0	10	2 US-08-456-112B-8	Sequence 8, Appl1
8	35	100.0	10	2 US-08-456-112B-41	Sequence 8, Appl1
9	35	100.0	11	1 US-08-049-871-8	Sequence 8, Appl1
10	35	100.0	11	1 US-07-819-893-8	Sequence 8, Appl1
11	35	100.0	11	1 US-08-280-397-8	Sequence 8, Appl1
12	35	100.0	11	2 US-08-456-112B-37	Sequence 37, Appl1
13	35	100.0	12	1 US-08-097-830E-20	Sequence 20, Appl1
14	35	100.0	12	2 US-08-456-112B-20	Sequence 20, Appl1
15	32	91.4	138	4 US-09-270-767-36351	Sequence 36351, A
16	32	91.4	138	4 US-09-270-767-51568	Sequence 51568, A
17	30	85.7	103	4 US-09-732-210-1231	Sequence 1231, Ap
18	30	85.7	114	4 US-09-540-236-1979	Sequence 1979, Ap
19	30	85.7	151	3 US-09-134-001C-5595	Sequence 5595, Ap
20	30	85.7	167	4 US-09-710-279-1802	Sequence 1802, Ap
21	30	85.7	219	4 US-09-583-110-5079	Sequence 5079, Ap
22	30	85.7	225	4 US-09-328-352-6504	Sequence 6504, Ap
23	30	85.7	289	3 US-09-627-376-4	Sequence 4, Appl1
24	30	85.7	289	4 US-10-047-676B-4	Sequence 4, Appl1
25	30	85.7	323	4 US-09-328-352-7120	Sequence 7120, Ap
26	30	85.7	360	4 US-09-949-016-10589	Sequence 10589, A
27	30	85.7	373	4 US-09-489-039A-8389	Sequence 8389, Ap

28	30	85.7	376	4 US-09-248-796A-16143	Sequence 16143, A
29	30	85.7	403	4 US-09-248-796A-14239	Sequence 14239, A
30	30	85.7	438	4 US-09-134-000C-4760	Sequence 4760, Ap
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32	29	82.9	208	4 US-09-248-796A-20557	Sequence 20557, A
33	29	82.9	323	4 US-09-248-796A-16328	Sequence 16328, A
34	29	82.9	555	4 US-09-489-039A-10752	Sequence 10752, A
35	28	80.0	73	4 US-09-328-352-4976	Sequence 27744, A
36	28	80.0	84	4 US-09-328-352-4976	Sequence 4976, Ap
37	28	80.0	95	4 US-09-270-767-57772	Sequence 57772, A
38	28	80.0	97	4 US-09-134-000C-4160	Sequence 4160, Ap
39	28	80.0	116	1 US-08-702-344-21	Sequence 21, Appl
40	28	80.0	132	4 US-09-270-767-44785	Sequence 44785, A
41	28	80.0	153	4 US-09-270-767-47648	Sequence 47648, A
42	28	80.0	154	4 US-09-134-000C-5197	Sequence 5197, Ap
43	28	80.0	259	4 US-09-902-540-16016	Sequence 16016, A
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46	28	80.0	342	4 US-09-489-039A-12340	Sequence 12340, A
47	28	80.0	503	4 US-09-248-796A-18992	Sequence 18992, A
48	28	80.0	538	4 US-09-270-767-44083	Sequence 44083, A
49	28	80.0	547	4 US-09-248-796A-19600	Sequence 19600, A
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51	28	80.0	718	3 US-09-346-237-10	Sequence 10, Appl
52	28	80.0	754	4 US-09-270-767-42479	Sequence 42479, A
53	28	80.0	867	4 US-09-417-485D-2	Sequence 2, Appl1
54	28	80.0	867	4 US-09-417-485D-4	Sequence 4, Appl1
55	28	80.0	887	1 US-08-215-709-1	Sequence 1, Appl1
56	28	80.0	892	4 US-09-489-039A-12282	Sequence 12282, A
57	28	80.0	1140	4 US-09-579-692B-8	Sequence 8, Appl1
58	27	77.1	9	2 US-08-456-112B-40	Sequence 40, Appl
59	27	77.1	10	1 US-08-097-830E-10	Sequence 10, Appl
60	27	77.1	10	2 US-08-456-112B-10	Sequence 10, Appl
61	27	77.1	20	3 US-08-940-424-9	Sequence 9, Appl1
62	27	77.1	58	4 US-09-621-976-7068	Sequence 7068, Ap
63	27	77.1	61	4 US-09-107-532A-7158	Sequence 7158, Ap
64	27	77.1	65	4 US-09-248-796A-24449	Sequence 24449, A
65	27	77.1	74	4 US-09-248-796A-25684	Sequence 25684, A
66	27	77.1	119	3 US-08-890-865A-17	Sequence 17, Appl
67	27	77.1	125	4 US-09-270-767-39180	Sequence 39180, A
68	27	77.1	125	4 US-09-270-767-54397	Sequence 54397, A
69	27	77.1	141	4 US-09-328-352-6351	Sequence 6351, Ap
70	27	77.1	166	4 US-09-270-767-36357	Sequence 36357, A
71	27	77.1	166	4 US-09-270-767-37478	Sequence 37478, A
72	27	77.1	173	4 US-09-270-767-51574	Sequence 51574, A
73	27	77.1	207	4 US-09-270-767-34523	Sequence 34523, A
74	27	77.1	235	4 US-09-248-796A-15246	Sequence 15246, A
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76	27	77.1	237	4 US-09-248-796A-21561	Sequence 21561, A
77	27	77.1	249	4 US-09-248-796A-20298	Sequence 20298, A
78	27	77.1	253	4 US-09-270-767-40298	Sequence 40298, A
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81	27	77.1	318	4 US-09-585-858-43	Sequence 43, Appl
82	27	77.1	318	4 US-10-270-878-43	Sequence 43, Appl
83	27	77.1	339	4 US-09-692-570-6	Sequence 6, Appl1
84	27	77.1	347	3 US-08-445-515-58	Sequence 58, Appl
85	27	77.1	348	3 US-08-445-515-56	Sequence 56, Appl
86	27	77.1	378	4 US-09-107-532A-4777	Sequence 4777, Ap
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88	27	77.1	400	4 US-09-438-185A-291	Sequence 291, App
89	27	77.1	420	5 PCR-US96-0825B-40	Sequence 40, Appl
90	27	77.1	420	5 PCR-US96-0825B-40	Sequence 40, Appl
91	27	77.1	438	4 US-09-248-796A-19601	Sequence 19601, A
92	27	77.1	536	4 US-09-248-796A-19601	Sequence 19601, A
93	27	77.1	536	4 US-09-328-352-5727	Sequence 5727, Ap
94	27	77.1	552	4 US-09-248-796A-15337	Sequence 15337, A
95	27	77.1	610	4 US-09-248-796A-17030	Sequence 17030, A
96	27	77.1	617	4 US-09-198-452A-155	Sequence 155, App
97	27	77.1	617	4 US-09-438-185A-138	Sequence 138, App
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OM protein - protein search, using sw model

Run on: March 26, 2005, 12:17:20 / Search time 47.9624 Seconds

(without alignments)
75.937 Million cell updates/sec

Title: US-09-124-280A-37

Perfect score: 54

Sequence: 1 IKFLKFLK 11

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	49	90.7	10	9	US-09-124-280A-11
5	42	77.8	209	16	US-10-437-963-147868
6	42	77.8	66	15	US-10-424-599-152246
7	40	74.1	9	15	US-10-247-4768-13
8	39	72.2	9	15	US-10-247-4768-13
9	39	72.2	256	15	US-10-282-122A-51850
10	38	70.4	10	9	US-09-124-280A-10
11	38	70.4	10	14	US-10-083-259-148
12	38	70.4	10	14	US-10-09-274A-148
13	38	70.4	10	15	US-10-176-419A-6

14	38	70.4	10	17	US-10-818-158-4	Sequence 4, App1
15	38	70.4	11	14	US-10-109-274A-20	Sequence 20, App1
16	38	70.4	11	15	US-10-240-641-28	Sequence 28, App1
17	38	70.4	23	15	US-10-176-419A-2	Sequence 2, App1
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19	37	68.5	248	15	US-10-424-599-265470	Sequence 265470, A
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21	37	68.5	476	15	US-10-282-122A-53100	Sequence 53100, A
22	37	68.5	1001	15	US-10-282-122A-53100	Sequence 10, App1
23	36	66.7	43	15	US-10-607-631-10	Sequence 285041, A
24	36	66.7	43	15	US-10-424-599-285041	Sequence 221561, A
25	36	66.7	45	15	US-10-424-599-221561	Sequence 38288, A
26	36	66.7	50	9	US-09-864-761-38298	Sequence 45310, A
27	36	66.7	94	15	US-10-425-114-45310	Sequence 58311, A
28	36	66.7	94	15	US-10-425-114-58311	Sequence 60122, A
29	36	66.7	94	15	US-10-425-114-60122	Sequence 61564, A
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33	36	66.7	208	15	US-10-282-122A-45253	Sequence 45253, A
34	36	66.7	228	15	US-10-425-114-70797	Sequence 70797, A
35	36	66.7	229	16	US-10-437-963-16745	Sequence 166745, A
36	36	66.7	415	9	US-09-815-242-5494	Sequence 5494, App
37	36	66.7	420	9	US-09-815-242-5494	Sequence 12649, A
38	36	66.7	420	11	US-09-930-512-28	Sequence 28, App1
39	36	66.7	420	15	US-10-282-122A-44436	Sequence 44436, A
40	36	66.7	420	15	US-10-282-122A-71626	Sequence 71626, A
41	36	66.7	420	17	US-10-857-625-799	Sequence 799, App
42	36	66.7	423	9	US-09-815-242-10678	Sequence 10678, A
43	36	66.7	957	16	US-10-437-963-167447	Sequence 167447, A
44	36	66.7	967	15	US-10-425-114-58755	Sequence 58755, A
45	36	66.7	967	15	US-10-425-114-62853	Sequence 62853, A
46	35	64.8	7	9	US-09-124-280A-37	Sequence 7, App1
47	35	64.8	7	9	US-09-124-280A-37	Sequence 38, App1
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51	35	64.8	418	15	US-10-282-122A-57481	Sequence 57481, A
52	35	64.8	420	15	US-10-282-122A-57062	Sequence 57062, A
53	35	64.8	1279	15	US-09-883-227-188	Sequence 188, App
54	34	63.0	47	15	US-10-424-599-149057	Sequence 149057, A
55	34	63.0	65	15	US-10-424-599-203343	Sequence 203343, A
56	34	63.0	73	9	US-09-864-761-41602	Sequence 41602, A
57	34	63.0	77	15	US-10-424-599-198418	Sequence 198418, A
58	34	63.0	101	15	US-10-424-599-227181	Sequence 227181, A
59	34	63.0	106	15	US-10-424-599-200324	Sequence 200324, A
60	34	63.0	243	15	US-10-425-114-46311	Sequence 46311, A
61	34	63.0	258	15	US-10-424-599-229486	Sequence 229486, A
62	34	63.0	445	15	US-10-282-122A-50132	Sequence 50132, A
63	34	63.0	873	15	US-10-369-493-6226	Sequence 6226, App
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66	33	61.1	8	14	US-10-109-274A-9	Sequence 9, App1
67	33	61.1	8	15	US-10-240-641-9	Sequence 40, App1
68	33	61.1	9	9	US-09-124-280A-40	Sequence 151, App
69	33	61.1	9	14	US-10-083-259-1	Sequence 152, App
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71	33	61.1	9	14	US-10-083-259-152	Sequence 151, App
72	33	61.1	9	14	US-10-109-274A-1	Sequence 152, App
73	33	61.1	9	14	US-10-109-274A-1	Sequence 8, App1
74	33	61.1	9	14	US-10-109-274A-151	Sequence 153, App
75	33	61.1	9	15	US-10-109-274A-153	Sequence 153, App
76	33	61.1	11	14	US-10-424-599-261977	Sequence 261977, A
77	33	61.1	11	14	US-10-424-599-261977	Sequence 170388, A
78	33	61.1	39	15	US-10-424-599-259314	Sequence 259314, A
79	33	61.1	42	15	US-10-424-599-273835	Sequence 273835, A
80	33	61.1	43	15	US-10-424-599-29370	Sequence 29370, A
81	33	61.1	45	14	US-10-029-386-29370	Sequence 34507, A
82	33	61.1	51	9	US-09-864-761-34507	Sequence 224286, A
83	33	61.1	51	15	US-10-424-599-224286	Sequence 1460, App
84	33	61.1	55	9	US-09-867-550-1460	Sequence 48052, A
85	33	61.1	71	15	US-10-425-114-48052	Sequence 243043, A
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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:54:27 ; Search time 18.7473 Seconds

(without alignments)
43.800 Million cell updates/sec

Title: US-09-124-280A-37
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Gap 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	54	100.0	11	1	US-08-456-112B-37
5	50	92.6	10	1	US-08-097-830E-8
6	50	92.6	10	1	US-08-456-112B-8
7	50	92.6	12	1	US-08-097-830E-20
8	50	92.6	12	2	US-08-456-112B-20
9	49	90.7	10	2	US-08-456-112B-41
10	40	74.1	10	4	US-09-248-796A-16944
11	38	70.4	10	1	US-08-097-830E-10
12	38	70.4	10	2	US-08-456-112B-10
13	38	70.4	10	2	US-09-489-039A-8389
14	37	68.5	421	4	US-09-710-279-1820
15	37	68.5	427	3	US-09-134-001C-5141
16	36	66.7	138	4	US-09-270-767-51568
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18	36	66.7	151	3	US-09-134-001C-5595
19	36	66.7	167	4	US-09-710-279-1802
20	36	66.7	225	3	US-09-328-352-5504
21	36	66.7	418	3	US-08-855-910-1111
22	36	66.7	433	4	US-09-134-000C-3686
23	36	66.7	532	4	US-09-248-796A-25337
24	35	64.8	7	1	US-07-819-893-9
25	35	64.8	7	1	US-08-280-397-9
26	35	64.8	7	1	US-08-097-830E-7
27	35	64.8	7	2	US-08-456-112B-7

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66	32	59.3	1113	4	US-09-959-392-4	Sequence 9707, Ap
67	32	59.3	1580	3	US-08-726-330-1	Sequence 4, Appl
68	32	59.3	1580	3	US-09-208-716-1	Sequence 1, Appl
69	32	59.3	1581	3	US-08-726-330-3	Sequence 3, Appl
70	32	59.3	1581	3	US-09-208-716-3	Sequence 49, Appl
71	31	57.4	17	1	US-07-725-331-99	Sequence 49, Appl
72	31	57.4	17	5	PCT-US91-05047-49	Sequence 3695, Ap
73	31	57.4	60	4	US-09-107-433-3695	Sequence 27013, A
74	31	57.4	62	4	US-09-248-796A-27013	Sequence 4459, Ap
75	31	57.4	74	4	US-09-513-999C-4459	Sequence 25778, A
76	31	57.4	81	4	US-09-513-999C-4459	Sequence 40056, A
77	31	57.4	92	4	US-09-248-796A-25778	Sequence 55772, A
78	31	57.4	92	4	US-09-270-767-40056	Sequence 60137, A
79	31	57.4	95	4	US-09-270-767-55272	Sequence 4160, Ap
80	31	57.4	97	4	US-09-270-767-60137	Sequence 5500, Ap
81	31	57.4	105	4	US-09-134-000C-4160	Sequence 8587, Ap
82	31	57.4	120	4	US-09-107-532A-5500	Sequence 46833, A
83	31	57.4	126	4	US-09-489-039A-8587	Sequence 36357, A
84	31	57.4	166	4	US-09-270-767-44683	Sequence 51574, A
85	31	57.4	166	4	US-09-270-767-36357	Sequence 36870, A
86	31	57.4	174	4	US-09-270-767-36870	Sequence 52087, A
87	31	57.4	174	4	US-09-270-767-52087	Sequence 57056, A
88	31	57.4	188	4	US-09-270-767-57056	Sequence 5079, Ap
89	31	57.4	229	4	US-09-283-110-5079	Sequence 45076, A
90	31	57.4	233	4	US-09-670-767-45076	Sequence 182, App
91	31	57.4	242	4	US-09-198-452A-182	Sequence 40298, A
92	31	57.4	253	4	US-09-270-767-40298	Sequence 55514, A
93	31	57.4	253	4	US-09-270-767-55514	Sequence 16033, A
94	31	57.4	279	4	US-09-248-796A-16033	Sequence 772, App
95	31	57.4	316	4	US-09-538-092-772	Sequence 15858, A
96	31	57.4	341	4	US-09-248-796A-15858	Sequence 164, App
97	31	57.4	356	4	US-09-439-261-19	Sequence 16143, A
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99	31	57.4	356	4	US-09-438-185A-164	
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OM protein - protein search, using sw model

Run on: March 26, 2005, 12:17:20 ; Search time 43.6021 Seconds
(without alignments)
75.937 Million cell updates/sec

Title: US-09-124-280a-36

Perfect score: 49

Sequence: 1 IKTKKFLKKT 10

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Database: Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	36	73.5	522	15	US-10-369-493-10083
5	36	73.5	636	13	US-10-005-057A-9
6	36	73.5	636	15	US-10-675-072A-10
7	36	73.5	818	15	US-10-425-114-41341
8	35	71.4	50	15	US-10-424-599-229375
9	35	71.4	90	15	US-10-424-599-177817
10	35	71.4	99	15	US-10-424-599-237913
11	35	71.4	107	16	US-10-437-963-111721
12	35	71.4	126	16	US-10-767-701-51490
13	35	71.4	129	15	US-10-424-599-187159

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15	35	71.4	137	15	US-10-424-599-143973	Sequence 143973,
16	35	71.4	221	16	US-10-767-701-55755	Sequence 55755, A
17	35	71.4	840	15	US-10-369-493-22262	Sequence 22262, A
18	35	71.4	1015	14	US-10-032-201B-182	Sequence 7162, Ap
19	35	71.4	1161	15	US-10-282-122A-47195	Sequence 47195, A
20	34	69.4	17	15	US-10-451-795-11	Sequence 11, Appl
21	34	69.4	70	15	US-10-424-599-190970	Sequence 190970,
22	34	69.4	76	15	US-10-424-599-147608	Sequence 147608,
23	34	69.4	203	16	US-10-437-963-138857	Sequence 138857,
24	34	69.4	230	16	US-10-182-960-6	Sequence 6, Appl
25	34	69.4	418	15	US-10-282-122A-46744	Sequence 46744, A
26	34	69.4	1193	15	US-10-452-024-92	Sequence 92, Appl
27	34	69.4	1193	15	US-10-452-024-93	Sequence 93, Appl
28	34	69.4	2022	16	US-10-408-765A-598	Sequence 598, Ap
29	33	68.4	11	9	US-09-124-280a-36	Sequence 35, Appl
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31	33	67.3	62	15	US-10-424-599-195872	Sequence 195872,
32	33	67.3	67	15	US-10-424-599-244529	Sequence 244529,
33	33	67.3	119	9	US-09-764-864-1015	Sequence 1015, Ap
34	33	67.3	119	9	US-09-939-980-327	Sequence 327, Appl
35	33	67.3	164	13	US-10-114-893-42	Sequence 42, Appl
36	33	67.3	260	15	US-10-282-122A-52346	Sequence 52346, A
37	33	67.3	373	15	US-10-282-122A-43721	Sequence 43721, A
38	33	67.3	404	15	US-10-369-493-1488	Sequence 1488, Ap
39	33	67.3	418	15	US-10-369-493-2920	Sequence 2920, Ap
40	33	67.3	481	15	US-10-282-122A-54206	Sequence 54206, A
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42	33	67.3	517	15	US-10-369-493-22098	Sequence 22098, A
43	33	67.3	566	15	US-10-349-852-3	Sequence 3, Appl
44	33	67.3	579	15	US-10-282-122A-45535	Sequence 45535, A
45	33	67.3	695	10	US-09-890-688-130	Sequence 130, App
46	33	67.3	1247	16	US-10-437-963-128984	Sequence 128984,
47	32	65.3	68	16	US-10-437-963-196147	Sequence 196147,
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50	32	65.3	97	15	US-10-424-599-243797	Sequence 243797,
51	32	65.3	99	15	US-10-424-599-172391	Sequence 172391,
52	32	65.3	99	16	US-10-437-963-115655	Sequence 115655,
53	32	65.3	108	9	US-09-071-838-172	Sequence 172, App
54	32	65.3	108	14	US-10-213-512-172	Sequence 172, App
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61	32	65.3	124	15	US-10-424-599-158167	Sequence 158167,
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67	32	65.3	130	16	US-10-437-963-147470	Sequence 147470,
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70	32	65.3	132	15	US-10-425-114-62986	Sequence 62986, A
71	32	65.3	132	15	US-10-425-114-72146	Sequence 72146, A
72	32	65.3	132	16	US-10-767-701-413353	Sequence 413353, A
73	32	65.3	139	9	US-09-925-300-1325	Sequence 1325, Ap
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75	32	65.3	143	15	US-10-425-114-40991	Sequence 40991, A
76	32	65.3	147	9	US-09-925-301-1129	Sequence 1129, Ap
77	32	65.3	149	15	US-10-264-049-3908	Sequence 3908, Ap
78	32	65.3	149	16	US-10-437-963-168467	Sequence 168467,
79	32	65.3	177	15	US-10-425-114-56471	Sequence 56471, A
80	32	65.3	183	15	US-10-425-114-56680	Sequence 56680, A
81	32	65.3	263	15	US-10-289-762-23	Sequence 23, Appl
82	32	65.3	263	9	US-09-946-406-6	Sequence 6, Appl
83	32	65.3	293	15	US-10-353-699-4	Sequence 6, Appl
84	32	65.3	293	16	US-10-684-978-6	Sequence 6, Appl
85	32	65.3	293	17	US-10-753-267-20	Sequence 20, Appl
86	32	65.3	298	9	US-09-815-242-13325	Sequence 13325, A

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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:54:27 ; Search time 17.043 Seconds

(without alignments)
43,800 Million cell updates/sec

Title: US-09-124-280A-36

Perfect score: 49

Sequence: 1 IKTKKFLVKKKT 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	49	100.0	10	1	US-08-218-026-48
5	49	100.0	10	2	US-08-653-632-48
6	49	100.0	10	2	US-08-456-112B-36
7	49	100.0	10	3	US-08-477-778-7
8	49	100.0	10	5	PCT-US94-01234-46
9	35	71.4	115	4	US-09-732-210-730-1
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11	34	69.4	288	4	US-09-270-767-40523
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13	33.5	68.4	11	1	US-08-049-871-6
14	33.5	68.4	11	1	US-07-819-893-6
15	33.5	68.4	11	1	US-08-280-397-6
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26	32	65.3	120	4	US-09-248-796A-19735
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37	32	65.3	298	4	US-09-583-110-3786	Sequence 3786, Ap
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88	31	63.3	32	1	US-08-457-798-16	Sequence 16, Appl
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91	31	63.3	32	1	US-08-457-171-22	Sequence 22, Appl
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93	31	63.3	32	2	US-08-505-486-22	Sequence 22, Appl
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97	31	63.3	32	3	US-08-801-028-22	Sequence 22, Appl
98	31	63.3	32	3	US-09-340-154-16	Sequence 16, Appl
99	31	63.3	32	3	US-09-340-154-22	Sequence 22, Appl
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OM protein - protein search, using SW model

Run on: March 26, 2005, 12:17:20 ; Search time 47.9624 Seconds
(without alignments)
75.937 Million cell updates/sec

Title: US-09-124-280A-35

Perfect score: 62

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Gapop 10.0, Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database: Published Applications AA:*

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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	100.0	11	9	US-09-124-280A-35
2	58	93.5	10	9	US-09-124-280A-31
3	58	93.5	13	15	US-10-451-795-10
4	58	93.5	14	15	US-10-451-795-8
5	58	93.5	17	15	US-10-451-795-7
6	58	93.5	17	15	US-10-451-795-7
7	58	93.5	17	15	US-10-451-795-7
8	58	93.5	17	15	US-10-451-795-7
9	58	93.5	17	15	US-10-451-795-7
10	58	93.5	17	15	US-10-451-795-7
11	58	93.5	17	15	US-10-451-795-7
12	58	93.5	17	15	US-10-451-795-7
13	58	93.5	17	15	US-10-451-795-7
14	58	93.5	17	15	US-10-451-795-7
15	58	93.5	17	15	US-10-451-795-7
16	58	93.5	17	15	US-10-451-795-7
17	58	93.5	17	15	US-10-451-795-7
18	58	93.5	17	15	US-10-451-795-7
19	58	93.5	17	15	US-10-451-795-7
20	58	93.5	17	15	US-10-451-795-7
21	58	93.5	17	15	US-10-451-795-7
22	58	93.5	17	15	US-10-451-795-7
23	58	93.5	17	15	US-10-451-795-7
24	58	93.5	17	15	US-10-451-795-7
25	58	93.5	17	15	US-10-451-795-7
26	58	93.5	17	15	US-10-451-795-7
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14	39	62.9	127	15	US-10-425-114-49746	Sequence 49746, A
15	39	62.9	150	15	US-10-424-599-154184	Sequence 154184, A
16	39	62.9	173	15	US-10-425-114-37537	Sequence 37537, A
17	39	62.9	201	15	US-10-424-599-188735	Sequence 188735, A
18	39	62.9	278	15	US-10-374-780A-8	Sequence 8, Appl1
19	39	62.9	278	15	US-10-374-780A-326	Sequence 226, Ap
20	39	62.9	278	15	US-10-412-699B-252	Sequence 252, App
21	39	62.9	283	15	US-10-424-599-276904	Sequence 276904, A
22	39	62.9	284	15	US-10-425-114-72851	Sequence 72851, A
23	39	62.9	312	15	US-10-424-599-188732	Sequence 188732, A
24	39	62.9	475	16	US-10-437-963-157772	Sequence 157772, A
25	39	62.9	483	16	US-10-437-963-193808	Sequence 193808, A
26	39	62.9	700	10	US-09-906-418-17	Sequence 17, Appl1
27	39	62.9	700	14	US-10-119-136-17	Sequence 17, Appl1
28	39	62.9	700	14	US-10-119-136-17	Sequence 17, Appl1
29	39	62.9	700	15	US-10-410-031-17	Sequence 17, Appl1
30	39	62.9	700	15	US-10-410-031-17	Sequence 17, Appl1
31	39	62.9	87	16	US-10-437-963-12824	Sequence 12824, A
32	39	62.9	135	15	US-10-320-797-3007	Sequence 3007, Ap
33	39	62.9	347	15	US-10-282-122A-47197	Sequence 47197, A
34	39	62.9	398	15	US-10-282-122A-52673	Sequence 52673, A
35	39	62.9	994	16	US-10-437-963-119823	Sequence 119823, A
36	39	62.9	2695	16	US-10-408-765A-1108	Sequence 1108, Ap
37	39	62.9	2749	14	US-10-227-338-4	Sequence 338, Ap
38	37.5	60.5	55	9	US-09-764-877-1345	Sequence 1345, Ap
39	37.5	60.5	55	15	US-10-242-515-1345	Sequence 1345, Ap
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41	37	59.7	10	9	US-09-124-280A-17	Sequence 17, Appl1
42	37	59.7	78	15	US-10-424-599-260019	Sequence 260019, A
43	37	59.7	181	15	US-10-425-114-53475	Sequence 53475, A
44	37	59.7	212	15	US-10-410-031-161	Sequence 161, App
45	37	59.7	212	15	US-10-410-031-161	Sequence 161, App
46	37	59.7	382	9	US-09-828-644-82	Sequence 82, Appl1
47	37	59.7	492	14	US-10-282-122A-73650	Sequence 73650, A
48	37	59.7	521	16	US-10-007-280A-212	Sequence 212, App
49	37	59.7	521	16	US-10-767-701-45538	Sequence 45538, A
50	37	59.7	524	15	US-10-425-114-57859	Sequence 57859, A
51	37	59.7	580	15	US-10-415-187-1	Sequence 1, Appl1
52	37	59.7	694	15	US-10-425-114-39401	Sequence 39401, A
53	37	59.7	701	16	US-10-437-963-107364	Sequence 107364, A
54	37	59.7	714	15	US-10-425-114-50040	Sequence 50040, A
55	37	59.7	975	16	US-10-437-963-186445	Sequence 186445, A
56	37	59.7	1003	16	US-10-437-963-181404	Sequence 181404, A
57	37	59.7	65	15	US-10-424-599-253240	Sequence 253240, A
58	37	59.7	80	15	US-10-424-599-244313	Sequence 244313, A
59	37	59.7	82	15	US-10-425-114-43438	Sequence 43438, A
60	37	59.7	106	16	US-10-437-963-195263	Sequence 195263, A
61	37	59.7	132	15	US-10-424-599-153331	Sequence 153331, A
62	37	59.7	139	16	US-10-767-701-44948	Sequence 44948, A
63	37	59.7	143	15	US-10-282-122A-53023	Sequence 53023, A
64	37	59.7	155	15	US-10-425-114-39066	Sequence 39066, A
65	37	59.7	156	15	US-10-424-599-278312	Sequence 278312, A
66	37	59.7	156	15	US-10-424-599-282921	Sequence 282921, A
67	37	59.7	221	15	US-10-335-977-7345	Sequence 7345, Ap
68	37	59.7	224	15	US-10-410-031-168	Sequence 168, App
69	37	59.7	256	16	US-10-437-963-111407	Sequence 111407, A
70	37	59.7	262	15	US-10-425-114-67855	Sequence 67855, A
71	37	59.7	278	16	US-10-437-963-124354	Sequence 124354, A
72	37	59.7	285	15	US-10-310-154-576	Sequence 576, App
73	37	59.7	287	15	US-10-424-599-149174	Sequence 149174, A
74	37	59.7	292	16	US-10-437-963-127100	Sequence 127100, A
75	37	59.7	303	15	US-10-425-114-62107	Sequence 62107, A
76	37	59.7	303	15	US-10-425-114-62108	Sequence 62108, A
77	37	59.7	303	15	US-10-425-114-63741	Sequence 63741, A
78	37	59.7	327	15	US-10-425-114-63741	Sequence 63741, A
79	37	59.7	334	15	US-10-425-114-63742	Sequence 63742, A
80	37	59.7	335	15	US-10-425-114-64589	Sequence 64589, A
81	37	59.7	336	10	US-09-374-064A-42	Sequence 42, Appl1
82	37	59.7	336	15	US-10-616-263-32	Sequence 2, Appl1
83	37	59.7	445	14	US-10-242-943-2	Sequence 58, Appl1
84	37	59.7	445	15	US-10-354-358-58	Sequence 30, Appl1

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OM protein - protein search, using SW model

Run on: March 26, 2005, 10:54:27 ; Search time 18.7473 Seconds
(Without alignments)
43,800 Million cell updates/sec

Title: US-09-124-280A-35
Perfect score: 62
Sequence: 1 IKTKCKFLKCC 11

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database : Issued Patents AA:*

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3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/6C_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	100.0	11	US-08-049-871-6	Sequence 6, Appli
2	62	100.0	11	US-07-819-893-6	Sequence 6, Appli
3	62	100.0	11	US-08-280-397-6	Sequence 6, Appli
4	62	100.0	11	US-08-456-112B-35	Sequence 35, Appli
5	58	93.5	10	US-08-049-871-2	Sequence 2, Appli
6	58	93.5	10	US-07-819-893-2	Sequence 2, Appli
7	58	93.5	10	US-08-280-397-2	Sequence 2, Appli
8	58	93.5	10	US-08-218-026-49	Sequence 49, Appli
9	58	93.5	10	US-08-653-632-49	Sequence 49, Appli
10	58	93.5	10	US-08-456-112B-31	Sequence 31, Appli
11	58	93.5	11	US-08-218-026-50	Sequence 50, Appli
12	58	93.5	11	US-08-653-632-50	Sequence 50, Appli
13	43	69.4	7	US-08-049-871-1	Sequence 1, Appli
14	43	69.4	7	US-07-819-893-1	Sequence 1, Appli
15	43	69.4	7	US-08-280-397-1	Sequence 1, Appli
16	43	69.4	7	US-08-456-112B-30	Sequence 30, Appli
17	41	66.1	209	US-09-107-433-4694	Sequence 4694, Ap
18	41	66.1	210	US-09-107-433-4694	Sequence 4694, Ap
19	40	64.5	185	US-09-270-767-60044	Sequence 60044, A
20	40	64.5	253	US-09-270-767-44597	Sequence 44597, A
21	39	62.9	147	US-09-640-211A-682	Sequence 682, App
22	38	61.3	37	US-08-858-207A-529	Sequence 529, App
23	38	61.3	355	US-09-270-767-37109	Sequence 37109, A
24	38	61.3	355	US-09-270-767-37109	Sequence 37109, A
25	38	61.3	355	US-09-270-767-37109	Sequence 37109, A
26	38	61.3	355	US-09-270-767-37109	Sequence 37109, A
27	37	59.7	10	US-08-097-830E-15	Sequence 15, Appli

28	37	59.7	10	US-08-097-830E-17	Sequence 17, Appli
29	37	59.7	10	US-08-456-112B-15	Sequence 15, Appli
30	37	59.7	10	US-08-456-112B-17	Sequence 17, Appli
31	37	59.7	20	US-09-615-153-5	Sequence 5, Appli
32	37	59.7	112	US-09-270-767-39668	Sequence 39668, A
33	37	59.7	112	US-09-270-767-39668	Sequence 39668, A
34	37	59.7	168	US-09-270-767-43330	Sequence 43330, A
35	36	58.1	144	US-09-328-352-6468	Sequence 6468, Ap
36	36	58.1	445	US-09-167-206-2	Sequence 2, Appli
37	36	58.1	445	US-09-538-092-1181	Sequence 1181, Ap
38	36	58.1	490	US-09-949-016-7829	Sequence 7829, Ap
39	35	57.3	204	US-09-904-615-117	Sequence 117, App
40	35	57.3	299	US-09-904-615-73	Sequence 142, App
41	35	57.3	307	US-09-904-615-142	Sequence 6, Appli
42	35	56.5	18	US-09-493-211-6	Sequence 7, Appli
43	35	56.5	18	US-09-493-211-7	Sequence 5832, A
44	35	56.5	111	US-09-270-767-58632	Sequence 6640, Ap
45	35	56.5	113	US-09-621-976-6640	Sequence 38027, A
46	35	56.5	123	US-09-270-767-38027	Sequence 53244, A
47	35	56.5	138	US-09-270-767-53244	Sequence 36820, A
48	35	56.5	138	US-09-270-767-16828	Sequence 52045, A
49	35	56.5	165	US-09-270-767-52045	Sequence 281, App
50	35	56.5	171	US-09-489-847-281	Sequence 2, Appli
51	35	56.5	171	US-08-934-939-2	Sequence 11174, A
52	35	56.5	171	US-09-270-767-36218	Sequence 43465, A
53	35	56.5	171	US-09-270-767-35113	Sequence 6661, Ap
54	35	56.5	171	US-10-083-720A-2	Sequence 43289, A
55	35	56.5	183	US-09-489-847-136	Sequence 8033, Ap
56	35	56.5	217	US-09-949-016-11174	Sequence 4436, Ap
57	35	56.5	218	US-09-270-767-43465	Sequence 373, App
58	35	56.5	235	US-09-949-016-6661	Sequence 4141, Ap
59	35	56.5	420	US-09-270-767-43289	Sequence 5006, Ap
60	35	56.5	439	US-09-328-352-8033	Sequence 45113, A
61	34	54.8	101	US-09-621-976-4436	Sequence 54195, A
62	34	54.8	137	US-08-858-207A-373	Sequence 14903, A
63	34	54.8	137	US-08-583-110-4141	Sequence 15931, A
64	34	54.8	138	US-09-107-433-5006	Sequence 51148, A
65	34	54.8	195	US-09-270-767-45113	Sequence 51148, A
66	34	54.8	261	US-09-270-767-38978	Sequence 44113, A
67	34	54.8	261	US-09-270-767-54195	Sequence 54195, A
68	34	54.8	310	US-09-248-796A-14903	Sequence 14903, A
69	34	54.8	323	US-09-270-767-55931	Sequence 15931, A
70	34	54.8	323	US-08-270-767-51148	Sequence 51148, A
71	34	54.8	335	US-09-538-092-811	Sequence 811, App
72	34	54.8	343	US-09-745-842-2	Sequence 2, Appli
73	34	54.8	355	US-09-803-286A-12	Sequence 12, Appli
74	34	54.8	365	US-09-270-767-44316	Sequence 44316, A
75	34	54.8	366	US-08-991-677-6	Sequence 6, Appli
76	34	54.8	392	US-09-270-767-59034	Sequence 59034, A
77	34	54.8	416	US-09-228-246-4	Sequence 4, Appli
78	34	54.8	472	US-09-270-767-43652	Sequence 4652, A
79	34	54.8	499	US-09-316-643A-8	Sequence 8, Appli
80	34	54.8	509	US-08-328-322-19	Sequence 19, Appli
81	34	54.8	553	US-08-328-322-19	Sequence 19, Appli
82	34	54.8	553	US-09-538-092-585	Sequence 585, App
83	34	54.8	665	US-09-270-767-42014	Sequence 42014, A
84	34	54.8	903	US-09-252-991A-17937	Sequence 17937, A
85	34	54.8	1014	US-09-762-724-2	Sequence 2, Appli
86	34	54.8	1824	US-08-680-327-3	Sequence 3, Appli
87	34	54.8	1824	US-09-328-246-2	Sequence 2, Appli
88	33.5	54.0	10	US-08-049-871-7	Sequence 7, Appli
89	33.5	54.0	10	US-07-819-893-7	Sequence 7, Appli
90	33.5	54.0	10	US-08-280-397-7	Sequence 7, Appli
91	33.5	54.0	10	US-08-456-112B-36	Sequence 48, Appli
92	33.5	54.0	10	US-08-653-632-48	Sequence 48, Appli
93	33.5	54.0	10	US-08-456-112B-36	Sequence 36, Appli
94	33.5	54.0	10	US-08-477-778-7	Sequence 7, Appli
95	33.5	54.0	10	PCT-US94-01234-46	Sequence 16, Appli
96	33.5	53.2	10	US-08-097-830E-16	Sequence 16, Appli
97	33	53.2	10	US-08-456-112B-16	Sequence 16, Appli
98	33	53.2	71	US-09-328-352-5067	Sequence 5067, App
99	33	53.2	86	US-09-270-767-44796	Sequence 44796, A
100	33	53.2	137	US-09-270-767-32233	Sequence 32233, A

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OM protein - protein search, using SW model

Run on: March 26, 2005, 12:17:20 ; Search time 39.2419 Seconds

(without alignments)
75.937 Million cell updates/sec

Title: US-09-124-280A-34

Sequence: 1 CKKLKPKCT 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database :

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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	9	US-09-124-280A-34	Sequence 34, App1
2	53	100.0	10	US-09-124-280A-33	Sequence 33, App1
3	43	81.1	414	US-10-282-122A-54310	Sequence 43310, A
4	40	75.5	167	US-10-424-599-248944	Sequence 248944, A
5	40	75.5	150	US-10-425-114-69912	Sequence 69912, A
6	40	75.5	1551	US-09-864-761-35904	Sequence 35904, A
7	40	75.5	1882	US-10-087-192-330	Sequence 330, A
8	39	73.6	338	US-10-264-049-2546	Sequence 2546, App
9	39	73.6	481	US-09-764-864-979	Sequence 979, App
10	38	71.7	536	US-09-864-761-36148	Sequence 36148, A
11	38	71.7	599	US-10-108-260A-3964	Sequence 3964, App
12	38	71.7	688	US-10-112-944-470	Sequence 470, App
13	37	69.8	236	US-10-424-599-224113	Sequence 224113, A

14	37	69.8	381	US-10-401-324-48	Sequence 48, App1
15	37	69.8	397	US-10-401-324-43	Sequence 43, App1
16	37	69.8	402	US-10-369-493-1196	Sequence 1196, App
17	37	69.8	480	US-10-437-963-180101	Sequence 180101, A
18	37	69.8	540	US-10-104-047-3748	Sequence 3748, App
19	37	69.8	568	US-10-203-0528-7	Sequence 7, App1
20	36	67.9	19	US-09-776-724A-188	Sequence 188, App
21	36	67.9	58	US-10-437-963-162216	Sequence 162216, A
22	36	67.9	67	US-10-424-599-262669	Sequence 262669, A
23	36	67.9	102	US-10-437-963-178358	Sequence 178358, A
24	36	67.9	122	US-09-776-724A-185	Sequence 185, App
25	36	67.9	147	US-10-767-701-53685	Sequence 53685, A
26	36	67.9	176	US-10-767-701-37509	Sequence 37509, A
27	36	67.9	194	US-10-220-120-257	Sequence 257, App
28	36	67.9	302	US-10-425-114-65633	Sequence 65633, A
29	36	67.9	432	US-10-369-493-19911	Sequence 19911, A
30	36	67.9	792	US-10-437-963-134089	Sequence 134089, A
31	35	66.0	164	US-09-934-455-502	Sequence 502, App
32	35	66.0	154	US-10-374-780A-2200	Sequence 2200, App
33	35	66.0	170	US-09-934-455-464	Sequence 464, App
34	35	66.0	170	US-10-374-780A-2156	Sequence 2156, App
35	35	66.0	426	US-10-221-625-5	Sequence 5, App1
36	35	66.0	426	US-10-104-047-3675	Sequence 3675, App
37	35	66.0	436	US-10-108-260A-4174	Sequence 4174, App
38	35	66.0	610	US-10-094-749-2804	Sequence 2804, App
39	35	66.0	610	US-10-108-260A-3772	Sequence 3772, App
40	35	66.0	728	US-10-408-765A-740	Sequence 740, App
41	35	66.0	909	US-10-479-435-28	Sequence 28, App1
42	35	66.0	2783	US-09-816-669A-14	Sequence 14, App1
43	35	66.0	2789	US-10-408-765A-2228	Sequence 2228, App
44	34.5	65.1	579	US-10-328-675A-6	Sequence 6, App1
45	34.5	65.1	931	US-10-436-715-61	Sequence 61, App1
46	34	64.2	73	US-10-424-599-273293	Sequence 273293, A
47	34	64.2	78	US-10-437-963-116168	Sequence 116168, A
48	34	64.2	132	US-10-437-963-137928	Sequence 137928, A
49	34	64.2	228	US-10-437-963-116774	Sequence 116774, A
50	34	64.2	228	US-10-424-599-157317	Sequence 157317, A
51	34	64.2	225	US-10-369-493-11992	Sequence 11992, A
52	34	64.2	221	US-09-764-864-961	Sequence 961, App
53	34	64.2	21	US-10-437-963-156455	Sequence 156455, A
54	34	64.2	281	US-09-764-864-1076	Sequence 1076, App
55	34	64.2	338	US-10-424-599-167507	Sequence 167507, A
56	34	64.2	333	US-10-424-599-197961	Sequence 197961, A
57	34	64.2	333	US-10-425-114-55856	Sequence 55856, A
58	34	64.2	33	US-09-864-761-42897	Sequence 42897, A
59	34	64.2	513	US-10-479-435-23	Sequence 23, App1
60	34	64.2	581	US-10-221-625-21	Sequence 21, App1
61	34	64.2	602	US-10-424-599-168193	Sequence 168193, A
62	34	64.2	644	US-10-408-765A-1196	Sequence 1196, App
63	34	64.2	902	US-10-029-386-32110	Sequence 32110, A
64	34	64.2	1191	US-10-408-765A-2105	Sequence 2105, App
65	34	64.2	1193	US-10-437-963-185505	Sequence 185505, A
66	34	64.2	2735	US-10-437-963-182452	Sequence 182452, A
67	33	62.3	51	US-10-424-599-147159	Sequence 147159, A
68	33	62.3	66	US-10-424-599-266601	Sequence 266601, A
69	33	62.3	174	US-10-424-599-153350	Sequence 153350, A
70	33	62.3	179	US-10-424-599-216417	Sequence 216417, A
71	33	62.3	183	US-09-764-864-949	Sequence 949, App1
72	33	62.3	193	US-09-862-540-45	Sequence 45, App1
73	33	62.3	287	US-09-764-864-934	Sequence 934, App1
74	33	62.3	292	US-10-466-164-49	Sequence 49, App1
75	33	62.3	294	US-10-186-886-22	Sequence 22, App1
76	33	62.3	298	US-10-425-114-67319	Sequence 47319, A
77	33	62.3	303	US-09-864-761-36091	Sequence 36091, A
78	33	62.3	311	US-10-437-963-156670	Sequence 156670, A
79	33	62.3	319	US-10-109-749-2144	Sequence 2144, App
80	33	62.3	353	US-10-104-047-2384	Sequence 2384, App
81	33	62.3	362	US-10-363-829-279	Sequence 279, App
82	33	62.3	391	US-10-437-963-171457	Sequence 171457, A
83	33	62.3	407	US-10-363-829-166	Sequence 366, App
84	33	62.3	416	US-10-029-386-13849	Sequence 33849, A
85	33	62.3	487	US-10-408-765A-425	Sequence 425, App
86	33	62.3	522		

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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:54:27 ; Search time 15.3387 Seconds

(without alignments)
43.800 Million cell updates/sec

Title: US-09-124-280a-34

Perfect score: 53 CKKLFCKRT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	9	1	US-08-049-871-5
2	53	100.0	9	1	US-07-819-893-5
3	53	100.0	9	1	US-08-280-397-5
4	53	100.0	9	2	US-08-456-112B-34
5	53	100.0	10	1	US-08-049-871-4
6	53	100.0	10	1	US-07-819-893-4
7	53	100.0	10	1	US-08-280-397-4
8	53	100.0	10	2	US-08-456-112B-33
9	39	73.6	803	4	US-09-538-092-1026
10	37	69.8	381	4	US-09-686-583B-48
11	37	69.8	397	4	US-09-686-583B-43
12	35	66.0	167	4	US-09-328-352-6844
13	35	66.0	395	3	US-09-032-372-1
14	35	66.0	867	4	US-09-248-796A-19207
15	35	66.0	3730	4	US-09-949-016-6356
16	35	65.1	579	4	US-09-519-232-6
17	34	64.2	76	4	US-09-270-767-58397
18	34	64.2	53	4	US-09-248-796A-26403
19	34	64.2	140	4	US-09-270-767-32712
20	34	64.2	140	4	US-09-270-767-47929
21	34	64.2	393	4	US-09-270-767-43063
22	34	64.2	519	4	US-09-248-796A-18734
23	34	64.2	1191	4	US-09-949-016-6356
24	33	62.3	20	4	US-09-615-153-5
25	33	62.3	60	4	US-09-270-767-34498
26	33	62.3	60	4	US-09-270-767-49715
27	33	62.3	108	4	US-09-270-767-59740

28	33	62.3	359	4	US-09-949-016-7156	Sequence 7156, Ap
29	33	62.3	367	4	US-09-949-016-6722	Sequence 6722, Ap
30	33	62.3	405	4	US-09-949-016-9688	Sequence 9688, Ap
31	33	62.3	698	4	US-09-949-016-11419	Sequence 11419, A
32	33	62.3	971	3	US-09-112-450-2	Sequence 2, Appl1
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34	33	62.3	971	4	US-10-116-048-2	Sequence 2, Appl1
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36	32	60.4	86	2	US-08-399-411-82	Sequence 82, Appl
37	32	60.4	86	3	US-08-516-859A-82	Sequence 82, Appl
38	32	60.4	86	3	US-09-586-472-82	Sequence 82, Appl
39	32	60.4	86	3	US-09-528-706-82	Sequence 82, Appl
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43	32	60.4	197	4	US-09-270-767-52546	Sequence 52546, A
44	32	60.4	330	4	US-09-543-681A-5940	Sequence 5940, Ap
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46	32	60.4	369	4	US-09-906-779-5	Sequence 5, Appl1
47	32	60.4	377	3	US-09-352-990-28	Sequence 6024, Ap
48	32	60.4	437	4	US-09-543-681A-6358	Sequence 6358, Ap
49	32	60.4	458	4	US-09-949-016-7581	Sequence 7581, Ap
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51	32	60.4	902	4	US-09-654-600A-10	Sequence 10, Appl
52	32	60.4	1141	1	US-08-363-300-2	Sequence 2, Appl1
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56	32	60.4	1706	3	US-09-586-472-2	Sequence 2, Appl1
57	32	60.4	1706	4	US-09-528-706-2	Sequence 2, Appl1
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59	31.5	59.4	10	2	US-08-456-112B-18	Sequence 18, Appl
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62	31	58.5	50	4	US-09-270-767-29403	Sequence 3403, A
63	31	58.5	50	4	US-09-270-767-54620	Sequence 54620, A
64	31	58.5	61	4	US-09-248-796A-26746	Sequence 3688, Ap
65	31	58.5	63	4	US-09-583-110-3688	Sequence 4050, A
66	31	58.5	122	4	US-09-107-433-4050	Sequence 27508, A
67	31	58.5	125	4	US-09-248-796A-27508	Sequence 75, Appl
68	31	58.5	125	4	US-09-216-393B-75	Sequence 12273, A
69	31	58.5	130	2	US-08-851-188-1	Sequence 1, Appl1
70	31	58.5	130	2	US-08-851-188-1	Sequence 1, Appl1
71	31	58.5	150	2	US-08-851-188-3	Sequence 3, Appl1
72	31	58.5	150	3	US-09-255-045-1	Sequence 3, Appl1
73	31	58.5	150	3	US-09-255-045-3	Sequence 645, Ap
74	31	58.5	150	4	US-09-949-016-6245	Sequence 9286, Ap
75	31	58.5	158	4	US-09-949-016-9986	Sequence 4490, Ap
76	31	58.5	163	4	US-09-134-000C-4490	Sequence 163, Ap
77	31	58.5	189	4	US-09-198-452A-183	Sequence 1754, A
78	31	58.5	189	4	US-09-438-185A-165	Sequence 5260, Ap
79	31	58.5	191	4	US-09-489-039A-13754	Sequence 5802, A
80	31	58.5	213	3	US-09-134-001C-5360	Sequence 2, Appl1
81	31	58.5	251	4	US-09-270-767-58802	Sequence 33109, A
82	31	58.5	272	4	US-09-686-583B-2	Sequence 43449, A
83	31	58.5	335	4	US-09-270-767-52326	Sequence 11256, A
84	31	58.5	355	4	US-09-270-767-52326	Sequence 30, Appl
85	31	58.5	408	4	US-09-270-767-43449	Sequence 34532, A
86	31	58.5	422	4	US-09-341-646B-10	Sequence 49749, A
87	31	58.5	438	4	US-09-248-796A-22527	Sequence 7, Appl1
88	31	58.5	444	4	US-09-949-016-11256	Sequence 16064, A
89	31	58.5	517	3	US-09-457-040B-14	Sequence 8, Appl1
90	31	58.5	536	4	US-09-549-519-30	Sequence 2, Appl1
91	31	58.5	536	4	US-09-549-519-30	Sequence 10194, A
92	31	58.5	536	4	US-09-270-767-34532	Sequence 6885, Ap
93	31	58.5	536	4	US-09-270-767-49749	Sequence 7130, Ap
94	31	58.5	650	4	US-08-207-954-7	Sequence 3, Appl1
95	31	58.5	728	4	US-09-248-796A-16064	
96	31	58.5	765	4	US-09-886-312A-8	
97	31	58.5	944	3	US-09-449-283A-2	
98	31	58.5	1125	4	US-09-949-016-10194	
99	31	58.5	1214	4	US-09-949-016-6885	
100	30.5	57.5	1318	4	US-09-949-016-7130	
			886	3	US-09-110-116-3	

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OW protein - protein search, using SW model

Run on: March 26, 2005, 12:17:20 ; Search time 43.6021 Seconds
(without alignments)
75.937 Million cell updates/sec

Title: US-09-124-280A-33
Perfect score: 58
Sequence: 1 CKLFCCKTK 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1407402 seqs, 331100923 residues
Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database:

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
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- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	58	100.0	10	US-09-124-280A-33	Sequence 33, Appl
2	53	91.4	9	US-09-124-280A-34	Sequence 34, Appl
3	43	74.1	15	US-10-282-122A-54310	Sequence 54310, A
4	43	74.1	1551	US-09-864-761-35904	Sequence 35904, A
5	43	74.1	1882	US-10-087-192-330	Sequence 330, App
6	40	69.0	167	US-10-424-599-248944	Sequence 248944, A
7	40	69.0	290	US-10-425-114-69912	Sequence 69912, A
8	39	67.2	338	US-10-264-049-2546	Sequence 2546, Ap
9	39	67.2	481	US-09-764-864-979	Sequence 979, App
10	38	65.5	536	US-09-864-761-35148	Sequence 35148, A
11	38	65.5	599	US-10-108-260A-3964	Sequence 3964, Ap
12	38	65.5	688	US-10-112-944-470	Sequence 470, App
13	37	63.8	179	US-10-424-599-216417	Sequence 216417, A

14	37	63.8	236	US-10-424-599-224113	Sequence 224113, A
15	37	63.8	381	US-10-401-324-48	Sequence 48, Appl
16	37	63.8	397	US-10-401-324-43	Sequence 43, Appl
17	37	63.8	402	US-10-369-493-1196	Sequence 1196, Ap
18	37	63.8	480	US-10-437-963-180101	Sequence 180101, A
19	37	63.8	540	US-10-104-047-3748	Sequence 3748, Ap
20	37	63.8	568	US-10-203-052B-7	Sequence 7, Appl
21	36	62.1	58	US-09-776-724A-188	Sequence 188, App
22	36	62.1	19	US-10-437-963-162216	Sequence 162216, A
23	36	62.1	67	US-10-424-599-262669	Sequence 262669, A
24	36	62.1	102	US-10-437-963-178358	Sequence 178358, A
25	36	62.1	122	US-09-776-724A-185	Sequence 185, App
26	36	62.1	147	US-10-767-701-53685	Sequence 53685, A
27	36	62.1	176	US-10-767-701-37509	Sequence 37509, A
28	36	62.1	194	US-10-220-120-257	Sequence 257, App
29	36	62.1	228	US-10-437-963-116774	Sequence 116774, A
30	36	62.1	302	US-10-425-114-65633	Sequence 65633, A
31	36	62.1	492	US-10-369-493-19911	Sequence 19911, A
32	36	62.1	792	US-10-437-963-134089	Sequence 134089, A
33	36	62.1	856	US-10-437-963-184883	Sequence 184883, A
34	36	62.1	996	US-10-437-963-187715	Sequence 187715, A
35	35	60.3	164	US-09-934-455-502	Sequence 502, App
36	35	60.3	164	US-10-374-780A-2200	Sequence 2200, Ap
37	35	60.3	170	US-09-934-455-464	Sequence 464, App
38	35	60.3	170	US-10-374-780A-2156	Sequence 2156, Ap
39	35	60.3	340	US-10-437-963-108735	Sequence 108735, A
40	35	60.3	426	US-10-221-625-5	Sequence 5, Appl
41	35	60.3	428	US-10-104-047-3675	Sequence 3675, Ap
42	35	60.3	436	US-10-108-260A-4174	Sequence 4174, Ap
43	35	60.3	513	US-10-479-435-23	Sequence 23, Appl
44	35	60.3	610	US-10-094-749-2604	Sequence 2604, Ap
45	35	60.3	610	US-10-108-260A-3772	Sequence 3772, Ap
46	35	60.3	738	US-10-408-765A-740	Sequence 740, App
47	35	60.3	909	US-10-479-435-28	Sequence 28, Appl
48	35	60.3	2783	US-09-816-669A-14	Sequence 14, Appl
49	35	60.3	2968	US-10-408-765A-2228	Sequence 2228, Ap
50	35	60.3	2806	US-10-015-115-60	Sequence 60, Appl
51	35	60.3	2910	US-10-322-696-18	Sequence 18, Appl
52	35	60.3	2911	US-09-825-751A-68	Sequence 68, Appl
53	35	60.3	2911	US-10-295-027-162	Sequence 162, App
54	35	60.3	2911	US-10-408-765A-421	Sequence 421, App
55	34.5	59.5	579	US-10-328-675A-6	Sequence 6, Appl
56	34.5	59.5	931	US-10-436-715-61	Sequence 61, Appl
57	34	58.6	73	US-10-424-599-273293	Sequence 273293, A
58	34	58.6	78	US-10-437-963-161168	Sequence 161168, A
59	34	58.6	98	US-10-424-599-272810	Sequence 272810, A
60	34	58.6	118	US-09-738-626-5573	Sequence 5573, Ap
61	34	58.6	122	US-09-764-864-1499	Sequence 1499, Ap
62	34	58.6	122	US-10-437-963-137928	Sequence 137928, A
63	34	58.6	140	US-09-764-864-1077	Sequence 1077, Ap
64	34	58.6	239	US-10-424-599-157317	Sequence 157317, A
65	34	58.6	255	US-10-369-493-11992	Sequence 11992, A
66	34	58.6	261	US-09-764-864-961	Sequence 961, App
67	34	58.6	271	US-10-437-963-156425	Sequence 156425, A
68	34	58.6	281	US-09-764-864-1076	Sequence 1076, Ap
69	34	58.6	338	US-10-424-599-167507	Sequence 167507, A
70	34	58.6	353	US-10-424-599-197961	Sequence 197961, A
71	34	58.6	363	US-10-425-114-55856	Sequence 55856, A
72	34	58.6	492	US-09-864-761-42897	Sequence 42897, A
73	34	58.6	581	US-10-221-625-21	Sequence 21, Appl
74	34	58.6	586	US-10-104-047-3592	Sequence 3592, Ap
75	34	58.6	602	US-10-424-599-168193	Sequence 168193, A
76	34	58.6	628	US-10-112-944-450	Sequence 450, App
77	34	58.6	642	US-10-225-027-434	Sequence 434, App
78	34	58.6	644	US-10-408-765A-1186	Sequence 1186, Ap
79	34	58.6	758	US-10-282-122A-53985	Sequence 53985, A
80	34	58.6	902	US-10-029-386-22110	Sequence 32110, A
81	34	58.6	1191	US-10-408-765A-2105	Sequence 2105, App
82	34	58.6	1193	US-10-437-963-185505	Sequence 185505, A
83	34	58.6	1254	US-10-437-963-111885	Sequence 11885, A
84	34	58.6	1419	US-10-437-963-125464	Sequence 125464, A
85	34	58.6	1535	US-10-437-963-111886	Sequence 11886, A
86	34	58.6	1688	US-10-437-963-188596	Sequence 188596, A

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OM protein - protein search, using ew model

Run on: March 26, 2005, 10:54:27 ; Search time 17.043 Seconds
(without alignments)
43.800 Million cell updates/sec

Title: US-09-124-280a-33

Perfect score: 58
Sequence: 1 CKKFKCKTK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	58	100.0	10	1	US-08-280-397-4
4	58	100.0	10	2	US-08-456-1128-33
5	53	91.4	9	1	US-08-049-871-5
6	53	91.4	9	1	US-07-819-893-5
7	53	91.4	9	1	US-08-280-397-5
8	53	91.4	9	2	US-08-456-1128-34
9	39	67.2	803	4	US-09-538-092-1026
10	37	63.8	20	4	US-09-615-153-5
11	37	63.8	381	4	US-09-686-583B-48
12	37	63.8	397	4	US-09-686-583B-43
13	35	60.3	85	4	US-09-270-767-59074
14	35	60.3	122	4	US-09-248-796A-37508
15	35	60.3	167	4	US-09-328-352-6844
16	35	60.3	313	4	US-09-270-767-43688
17	35	60.3	355	4	US-09-270-767-37109
18	35	60.3	355	4	US-09-270-767-44567
19	35	60.3	395	4	US-09-032-372-1
20	35	60.3	867	4	US-09-248-796A-19207
21	35	60.3	3730	4	US-09-949-016-9908
22	34.5	59.5	161	4	US-09-270-767-60018
23	34.5	59.5	417	4	US-09-270-767-44567
24	34.5	59.5	579	4	US-09-519-232-6
25	34	58.6	53	4	US-09-270-767-58397
26	34	58.6	76	4	US-09-248-796A-26403
27	34	58.6	77	4	US-09-513-999C-7155

28	34	58.6	140	4	US-09-270-767-32712	Sequence 32712, A
29	34	58.6	140	4	US-09-270-767-47929	Sequence 47929, A
30	34	58.6	169	4	US-09-732-210-54	Sequence 54, Appl
31	34	58.6	304	4	US-09-248-796A-18885	Sequence 18885, A
32	34	58.6	333	2	US-08-379-556A-8	Sequence 8, Appl
33	34	58.6	359	4	US-09-949-016-7156	Sequence 7156, Ap
34	34	58.6	393	4	US-09-270-767-33063	Sequence 43063, A
35	34	58.6	519	4	US-09-248-796A-18734	Sequence 18734, A
36	34	58.6	1191	4	US-09-949-016-6356	Sequence 6356, Ap
37	33	56.9	60	4	US-09-270-767-34498	Sequence 34498, A
38	33	56.9	60	4	US-09-270-767-49715	Sequence 49715, A
39	33	56.9	79	4	US-09-904-615-167	Sequence 167, Ap
40	33	56.9	80	4	US-09-904-615-120	Sequence 120, Ap
41	33	56.9	108	4	US-09-270-767-59740	Sequence 59740, A
42	33	56.9	125	4	US-09-615-192A-336	Sequence 336, Ap
43	33	56.9	367	4	US-09-949-016-6722	Sequence 6722, Ap
44	33	56.9	405	4	US-09-949-016-9688	Sequence 9688, Ap
45	33	56.9	698	4	US-09-949-016-11419	Sequence 11419, A
46	33	56.9	971	3	US-09-112-450-2	Sequence 2, Appl
47	33	56.9	971	4	US-09-419-291A-2	Sequence 2, Appl
48	33	56.9	971	4	US-10-116-048-2	Sequence 2, Appl
49	33	56.9	1130	4	US-09-538-092-834	Sequence 834, Ap
50	33	56.9	1169	4	US-09-949-016-9630	Sequence 9630, Ap
51	33	56.9	2871	4	US-09-538-092-1076	Sequence 1076, Ap
52	32.5	56.0	601	4	US-09-949-016-9977	Sequence 9977, Ap
53	32	55.2	70	4	US-09-248-796A-22032	Sequence 22032, A
54	32	55.2	72	4	US-09-248-796A-22607	Sequence 22607, A
55	32	55.2	86	2	US-08-459-568-82	Sequence 82, Appl
56	32	55.2	86	2	US-08-399-411-82	Sequence 82, Appl
57	32	55.2	86	3	US-08-516-859A-82	Sequence 82, Appl
58	32	55.2	86	3	US-09-586-472-82	Sequence 82, Appl
59	32	55.2	86	4	US-09-528-706-82	Sequence 82, Appl
60	32	55.2	103	3	US-09-134-001C-3719	Sequence 3719, Ap
61	32	55.2	113	4	US-09-902-540-16057	Sequence 16057, A
62	32	55.2	135	4	US-09-270-767-62131	Sequence 62131, A
63	32	55.2	153	4	US-09-270-767-35298	Sequence 35298, A
64	32	55.2	153	4	US-09-270-767-50515	Sequence 50515, A
65	32	55.2	154	4	US-09-270-767-36528	Sequence 36528, A
66	32	55.2	154	4	US-09-270-767-51745	Sequence 51745, A
67	32	55.2	163	4	US-09-270-767-37276	Sequence 37276, A
68	32	55.2	163	4	US-09-270-767-52493	Sequence 52493, A
69	32	55.2	172	4	US-09-270-767-42406	Sequence 42406, A
70	32	55.2	197	4	US-09-270-767-37329	Sequence 37329, A
71	32	55.2	197	4	US-09-270-767-52546	Sequence 52546, A
72	32	55.2	207	4	US-09-328-352-5203	Sequence 5203, Ap
73	32	55.2	319	4	US-09-710-279-786	Sequence 786, Ap
74	32	55.2	321	3	US-09-134-001C-3900	Sequence 3900, Ap
75	32	55.2	330	4	US-09-543-681A-5940	Sequence 5940, Ap
76	32	55.2	369	4	US-09-906-779-5	Sequence 5, Appl
77	32	55.2	370	4	US-09-863-339A-2	Sequence 2, Appl
78	32	55.2	376	4	US-09-134-000C-6024	Sequence 6024, Ap
79	32	55.2	377	3	US-09-352-990-28	Sequence 28, Appl
80	32	55.2	437	4	US-09-543-681A-6338	Sequence 6358, Ap
81	32	55.2	458	4	US-09-949-016-7581	Sequence 7581, Ap
82	32	55.2	501	4	US-09-863-339A-1	Sequence 1, Appl
83	32	55.2	737	4	US-09-949-016-9368	Sequence 9368, Ap
84	32	55.2	902	4	US-09-644-600-10	Sequence 10, Appl
85	32	55.2	902	4	US-09-654-600A-10	Sequence 2, Appl
86	32	55.2	1141	1	US-08-363-300-2	Sequence 2, Appl
87	32	55.2	1706	2	US-08-459-568-2	Sequence 2, Appl
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89	32	55.2	1706	3	US-08-516-859A-2	Sequence 2, Appl
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91	32	55.2	1706	4	US-09-528-706-2	Sequence 2, Appl
92	31.5	54.3	10	1	US-08-097-830E-18	Sequence 18, Appl
93	31.5	54.3	10	2	US-08-456-112B-18	Sequence 18, Appl
94	31.5	54.3	971	2	US-08-724-344B-22	Sequence 22, Appl
95	31.5	54.3	971	3	US-09-270-984A-22	Sequence 22, Appl
96	31.5	54.3	971	3	US-09-177-431-8	Sequence 8, Appl
97	31	53.4	9	4	US-09-615-153-14	Sequence 14, Appl
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100	31	53.4	49	4	US-09-270-767-52134	Sequence 52134, A

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3M protein - protein search, using sw model

Run on: March 26, 2005, 12:17:20 ; Search time 26.1613 Seconds
(Without alignments)
75.937 Million cell updates/sec

Title: US-09-124-280a-32

Perfect score: 30

Sequence: 1 KFLPKT 6

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Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 33110923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	30	100.0	59	US-09-989-890-188
6	30	100.0	59	US-10-074-511-67
7	30	100.0	145	US-10-425-114-61892
8	30	100.0	145	US-10-425-114-66205
9	30	100.0	145	US-10-425-114-66468
10	30	100.0	145	US-10-425-114-67300
11	30	100.0	145	US-10-425-114-67358
12	30	100.0	145	US-10-425-114-67735
13	30	100.0	176	US-10-282-122a-44416

14	30	100.0	177	US-10-335-977-5606	Sequence 5606, App
15	30	100.0	221	US-10-767-701-55755	Sequence 5575, A
16	30	100.0	409	US-10-469-061A-42	Sequence 42, Appl
17	30	100.0	470	US-10-001-189-65	Sequence 65, Appl
18	30	100.0	569	US-10-424-599-217393	Sequence 217393,
19	30	100.0	568	US-10-424-599-230772	Sequence 230772,
20	30	100.0	626	US-10-425-114-41326	Sequence 41326, A
21	30	100.0	843	US-10-437-963-134152	Sequence 134152,
22	30	100.0	985	US-10-437-963-105070	Sequence 105070,
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24	28	93.3	182	US-10-424-599-166601	Sequence 166601,
25	28	93.3	371	US-10-437-963-122405	Sequence 122405,
26	28	93.3	535	US-10-474-776-327	Sequence 327, App
27	28	93.3	535	US-10-472-928-2714	Sequence 2714, App
28	28	93.3	537	US-10-369-493-22792	Sequence 22792, A
29	27	90.0	44	US-10-424-599-166499	Sequence 166499,
30	27	90.0	52	US-10-424-599-159745	Sequence 159745,
31	27	90.0	57	US-10-424-599-248202	Sequence 248202,
32	27	90.0	64	US-09-764-891-3432	Sequence 3432, App
33	27	90.0	64	US-10-437-963-187393	Sequence 187393,
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39	27	90.0	176	US-10-437-963-107635	Sequence 107635,
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41	27	90.0	195	US-10-389-866-472	Sequence 472, App
42	27	90.0	198	US-10-204-887-124	Sequence 124, App
43	27	90.0	245	US-10-437-963-133848	Sequence 133848,
44	27	90.0	253	US-10-389-566-901	Sequence 901, App
45	27	90.0	272	US-10-282-122a-54509	Sequence 54509, A
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51	27	90.0	1104	US-10-369-493-19087	Sequence 19087, A
52	27	90.0	1237	US-10-369-493-19968	Sequence 19968, A
53	27	90.0	1237	US-10-108-604-3795	Sequence 3795, App
54	27	90.0	3829	US-10-408-765A-849	Sequence 849, App
55	26	86.7	34	US-09-864-761-43257	Sequence 43257, A
56	26	86.7	38	US-10-437-963-173646	Sequence 173646,
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59	26	86.7	49	US-10-424-599-221243	Sequence 221243,
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61	26	86.7	68	US-10-424-599-154378	Sequence 154378,
62	26	86.7	74	US-10-424-599-27078	Sequence 27078,
63	26	86.7	81	US-10-437-963-137947	Sequence 137947,
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65	26	86.7	86	US-10-424-599-233158	Sequence 233158,
66	26	86.7	86	US-10-424-599-153071	Sequence 153071,
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68	26	86.7	105	US-10-296-115-821	Sequence 821, App
69	26	86.7	106	US-10-437-963-197374	Sequence 197374,
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76	26	86.7	237	US-10-369-493-1137	Sequence 1137, App
77	26	86.7	250	US-10-289-762-593	Sequence 593, App
78	26	86.7	268	US-10-424-599-224851	Sequence 224851,
79	26	86.7	270	US-09-764-868-822	Sequence 822, App
80	26	86.7	302	US-09-764-875-750	Sequence 750, App
81	26	86.7	302	US-10-112-273-271	Sequence 271, App
82	26	86.7	312	US-09-862-027-10	Sequence 10, Appl
83	26	86.7	325	US-09-764-868-798	Sequence 798, Appl
84	26	86.7	340	US-09-764-875-1053	Sequence 1053, App
85	26	86.7	340		
86	26	86.7	11	US-09-764-875-1053	

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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:54:27 ; Search time 10.2258 Seconds
(without alignments)
43.800 Million cell updates/sec

Title: US-09-124-280A-32

Perfect score: 30
Sequence: 1 KFLKKT 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA.*
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2: /cgn2_6/prodata/1/1aa/5B_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query #	Query length	DB ID	Description
1	30	100.0	6	1	US-08-049-871-3
2	30	100.0	6	1	US-07-819-893-3
3	30	100.0	6	1	US-08-280-397-3
4	30	100.0	6	1	US-08-097-8308-30
5	30	100.0	6	2	US-08-456-1128-32
6	30	100.0	7	1	US-08-097-8308-6
7	30	100.0	7	2	US-08-456-1128-6
8	30	100.0	10	1	US-08-049-871-7
9	30	100.0	10	1	US-07-819-893-7
10	30	100.0	10	1	US-08-280-397-7
11	30	100.0	10	1	US-08-218-026-48
12	30	100.0	10	2	US-08-653-632-48
13	30	100.0	10	2	US-08-456-1128-36
14	30	100.0	10	3	US-08-477-778-7
15	30	100.0	10	3	PCT-US94-01234-46
16	30	100.0	16	4	US-09-270-767-36082
17	30	100.0	16	4	US-09-270-767-51299
18	30	100.0	30	3	US-09-475-316A-72
19	30	100.0	30	4	US-09-107-640-72
20	30	100.0	34	4	US-09-107-632A-5664
21	28	93.3	30	4	US-09-543-681A-6867
22	28	93.3	90	4	US-09-270-767-42739
23	27	90.0	61	4	US-09-107-532A-4641
24	27	90.0	61	4	US-09-107-532A-4641
25	27	90.0	62	4	US-09-270-767-60328
26	27	90.0	65	4	US-09-107-532A-4640
27	27	90.0	73	4	US-09-134-000C-6531

28	27	90.0	84	3	US-09-134-001C-3443	Sequence 3443, Ap
29	27	90.0	235	4	US-09-107-532A-3775	Sequence 3775, Ap
30	27	90.0	289	4	US-09-270-767-44861	Sequence 44861, A
31	27	90.0	383	4	US-09-248-796A-16746	Sequence 16746, A
32	27	90.0	503	3	US-09-068-195-24	Sequence 24, Appl
33	27	90.0	2175	4	US-09-693-205A-8	Sequence 8, Appl
34	27	90.0	3829	4	US-09-693-205A-2	Sequence 2, Appl
35	27	90.0	3829	4	US-09-693-205A-16	Sequence 16, Appl
36	27	90.0	3830	4	US-09-693-205A-4	Sequence 4, Appl
37	26	86.7	148	4	US-09-270-767-18941	Sequence 58941, A
38	26	86.7	148	4	US-09-732-210-328	Sequence 328, App
39	26	86.7	155	4	US-09-270-767-35995	Sequence 35995, A
40	26	86.7	155	4	US-09-270-767-51212	Sequence 51212, A
41	26	86.7	177	4	US-09-270-767-40406	Sequence 40406, A
42	26	86.7	177	4	US-09-270-767-55622	Sequence 55622, A
43	26	86.7	268	4	US-09-198-452A-593	Sequence 593, App
44	26	86.7	310	4	US-09-270-767-43571	Sequence 43571, A
45	26	86.7	314	4	US-09-438-185A-555	Sequence 555, App
46	26	86.7	326	4	US-09-345-473B-10	Sequence 10, Appl
47	26	86.7	363	4	US-09-792-024-80	Sequence 80, Appl
48	26	86.7	521	4	US-09-962-834A-2	Sequence 2, Appl
49	26	86.7	521	4	US-09-851-873-103	Sequence 103, App
50	26	86.7	535	2	US-08-933-750C-20	Sequence 20, Appl
51	26	86.7	535	3	US-09-234-613-20	Sequence 20, Appl
52	26	86.7	535	4	US-09-023-942A-10	Sequence 10, Appl
53	26	86.7	562	4	US-09-949-016-7299	Sequence 7299, Ap
54	26	86.7	573	4	US-09-134-000C-5258	Sequence 5258, Ap
55	26	86.7	596	4	US-09-248-796A-18495	Sequence 18495, A
56	26	86.7	850	4	US-09-270-767-39495	Sequence 39495, A
57	26	86.7	850	4	US-09-270-767-54712	Sequence 54712, A
58	26	86.7	1173	4	US-09-248-796A-19313	Sequence 19313, A
59	26	86.7	1447	4	US-09-252-991A-21474	Sequence 21474, A
60	26	86.7	1447	3	US-09-376-330-17	Sequence 17, Appl
61	25	83.3	7	1	US-08-049-871-1	Sequence 1, Appl
62	25	83.3	7	1	US-08-049-871-1	Sequence 1, Appl
63	25	83.3	7	1	US-08-280-397-1	Sequence 1, Appl
64	25	83.3	7	2	US-08-456-1128-30	Sequence 30, Appl
65	25	83.3	10	1	US-08-049-871-2	Sequence 2, Appl
66	25	83.3	10	1	US-07-819-893-2	Sequence 2, Appl
67	25	83.3	10	1	US-08-280-397-2	Sequence 2, Appl
68	25	83.3	10	1	US-08-465-325-129	Sequence 129, App
69	25	83.3	10	1	US-08-218-026-49	Sequence 49, Appl
70	25	83.3	10	2	US-08-653-632-49	Sequence 49, Appl
71	25	83.3	10	2	US-08-456-1128-31	Sequence 31, Appl
72	25	83.3	10	3	US-09-115-737-129	Sequence 129, App
73	25	83.3	11	1	US-08-049-871-6	Sequence 6, Appl
74	25	83.3	11	1	US-07-819-893-6	Sequence 6, Appl
75	25	83.3	11	1	US-08-280-397-6	Sequence 6, Appl
76	25	83.3	11	1	US-08-218-026-50	Sequence 50, Appl
77	25	83.3	11	2	US-08-653-632-50	Sequence 50, Appl
78	25	83.3	11	2	US-08-456-1128-35	Sequence 35, Appl
79	25	83.3	14	2	US-08-338-882-3	Sequence 3, Appl
80	25	83.3	15	2	US-08-338-882-5	Sequence 5, Appl
81	25	83.3	15	2	US-08-338-882-5	Sequence 5, Appl
82	25	83.3	15	2	US-08-338-882-7	Sequence 7, Appl
83	25	83.3	15	2	US-08-338-882-7	Sequence 7, Appl
84	25	83.3	16	1	US-08-465-325-149	Sequence 149, App
85	25	83.3	16	2	US-08-338-882-4	Sequence 4, Appl
86	25	83.3	16	3	US-09-115-737-149	Sequence 149, App
87	25	83.3	18	4	US-09-493-211-6	Sequence 6, Appl
88	25	83.3	18	4	US-09-493-211-6	Sequence 6, Appl
89	25	83.3	21	1	US-07-965-663A-1	Sequence 1, Appl
90	25	83.3	21	1	US-07-965-663A-2	Sequence 2, Appl
91	25	83.3	21	1	US-07-965-663A-3	Sequence 3, Appl
92	25	83.3	21	1	US-07-965-663A-22	Sequence 22, Appl
93	25	83.3	21	1	US-07-965-663A-23	Sequence 23, Appl
94	25	83.3	22	1	US-07-965-663A-6	Sequence 6, Appl
95	25	83.3	22	1	US-07-965-663A-7	Sequence 7, Appl
96	25	83.3	22	1	US-07-965-663A-19	Sequence 19, Appl
97	25	83.3	22	1	US-07-965-663A-20	Sequence 20, Appl
98	25	83.3	22	1	US-07-965-663A-21	Sequence 21, Appl
99	25	83.3	22	1	US-08-282-030-4	Sequence 4, Appl
100	25	83.3	22	1	US-08-282-030-51	Sequence 51, Appl

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OM protein - protein search, using sw model

Run on: March 26, 2005, 12:17:20 ; Search time 43.6021 Seconds
(without alignments)

75.937 Million cell updates/sec

Title: US-09-124-280a-31

Perfect score: 58

Sequence: 1 KTKCKFKKCC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep.*
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6: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	58	100.0	14	15	US-10-451-795-8
5	58	100.0	17	15	US-10-451-795-9
6	53	91.4	10	15	US-10-451-795-7
7	47.5	81.9	17	15	US-10-451-795-11
8	46	79.3	19	15	US-10-425-114-4394
9	43	74.1	7	9	US-09-124-280a-30
10	43	74.1	483	16	US-10-437-963-193616
11	41	70.7	209	17	US-10-472-928-2578
12	39	67.2	106	15	US-10-424-599-276903
13	39	67.2	115	15	US-10-425-114-40064

14	39	67.2	127	15	US-10-425-114-49746	Sequence 49746, A
15	39	67.2	150	15	US-10-424-599-154184	Sequence 154184, A
16	39	67.2	173	15	US-10-425-114-37537	Sequence 37537, A
17	39	67.2	201	15	US-10-424-599-188735	Sequence 188735, A
18	39	67.2	278	15	US-10-225-068-8	Sequence 8, Appl1
19	39	67.2	278	15	US-10-374-780A-2326	Sequence 2326, App
20	39	67.2	278	15	US-10-412-6998-252	Sequence 252, App
21	39	67.2	283	15	US-10-424-599-276904	Sequence 276904, A
22	39	67.2	284	15	US-10-425-114-72851	Sequence 72851, A
23	39	67.2	312	15	US-10-424-599-188732	Sequence 188732, A
24	39	67.2	475	16	US-10-437-963-167772	Sequence 167772, A
25	39	67.2	483	16	US-10-437-963-193808	Sequence 193808, A
26	38	65.5	87	16	US-10-437-963-102824	Sequence 102824, A
27	38	65.5	700	10	US-09-906-419-17	Sequence 17, Appl1
28	38	65.5	700	14	US-10-119-136-130	Sequence 130, App
29	38	65.5	700	15	US-10-410-031-17	Sequence 17, Appl1
30	38	65.5	700	15	US-10-410-031-130	Sequence 130, App
31	38	65.5	994	16	US-10-437-963-119823	Sequence 119823, A
32	38	65.5	994	16	US-10-437-963-119823	Sequence 1345, Ap
33	37.5	64.7	55	9	US-09-764-877-1345	Sequence 1345, Ap
34	37.5	64.7	55	15	US-10-242-515-1345	Sequence 1345, Ap
35	37	63.8	10	9	US-09-124-280a-15	Sequence 15, Appl1
36	37	63.8	10	9	US-09-124-280a-17	Sequence 17, Appl1
37	37	63.8	78	15	US-10-424-599-260019	Sequence 260019, A
38	37	63.8	216	9	US-09-828-644-82	Sequence 82, Appl1
39	37	63.8	492	14	US-10-007-880A-212	Sequence 212, App
40	37	63.8	580	15	US-10-437-963-186445	Sequence 186445, A
41	37	63.8	975	16	US-10-437-963-181404	Sequence 181404, A
42	37	63.8	1003	16	US-10-425-114-443438	Sequence 443438, A
43	36	62.1	82	15	US-10-425-114-443438	Sequence 443438, A
44	36	62.1	139	16	US-10-767-701-44948	Sequence 44948, A
45	36	62.1	143	15	US-10-828-1224-53023	Sequence 53023, A
46	36	62.1	155	15	US-10-425-114-39066	Sequence 39066, A
47	36	62.1	156	15	US-10-424-599-289321	Sequence 289321, A
48	36	62.1	156	15	US-10-424-599-289321	Sequence 289321, A
49	36	62.1	156	15	US-10-425-114-55475	Sequence 55475, A
50	36	62.1	181	15	US-10-410-031-181	Sequence 181, App
51	36	62.1	212	15	US-10-437-963-111407	Sequence 111407, A
52	36	62.1	278	16	US-10-437-963-124354	Sequence 124354, A
53	36	62.1	285	15	US-10-310-154-576	Sequence 576, App
54	36	62.1	287	15	US-10-424-599-149174	Sequence 149174, A
55	36	62.1	292	16	US-10-437-963-127100	Sequence 127100, A
56	36	62.1	303	15	US-10-425-114-62107	Sequence 62107, A
57	36	62.1	303	15	US-10-425-114-62108	Sequence 62108, A
58	36	62.1	303	15	US-10-425-114-63741	Sequence 63741, A
59	36	62.1	327	15	US-10-425-114-63743	Sequence 63743, A
60	36	62.1	334	15	US-10-425-114-63742	Sequence 63742, A
61	36	62.1	347	15	US-10-282-1224-47197	Sequence 47197, A
62	36	62.1	355	15	US-10-425-114-64589	Sequence 64589, A
63	36	62.1	396	10	US-09-374-046A-42	Sequence 42, Appl1
64	36	62.1	445	15	US-10-616-263-42	Sequence 42, Appl1
65	36	62.1	445	14	US-10-354-358-58	Sequence 58, Appl1
66	36	62.1	445	14	US-10-425-114-57859	Sequence 57859, A
67	36	62.1	445	15	US-10-425-114-39401	Sequence 39401, A
68	36	62.1	694	15	US-10-437-963-107364	Sequence 107364, A
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70	36	62.1	1384	16	US-10-437-963-146054	Sequence 146054, A
71	36	62.1	204	9	US-09-739-254-117	Sequence 117, App
72	36	62.1	204	14	US-10-054-988-117	Sequence 117, App
73	36	62.1	299	9	US-09-739-254-73	Sequence 73, Appl1
74	36	62.1	299	9	US-09-904-615-73	Sequence 73, Appl1
75	36	62.1	299	14	US-10-054-988-73	Sequence 73, Appl1
76	36	62.1	299	14	US-09-739-254-142	Sequence 142, App
77	36	62.1	307	9	US-09-904-615-142	Sequence 142, App
78	35.5	61.2	307	14	US-10-054-988-142	Sequence 142, App
79	35.5	61.2	307	14	US-10-054-988-142	Sequence 142, App
80	35.5	61.2	307	14	US-10-054-988-142	Sequence 142, App
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82	35.5	61.2	307	14	US-10-054-988-142	Sequence 142, App
83	35.5	61.2	307	14	US-10-054-988-142	Sequence 142, App
84	35.5	61.2	307	14	US-10-054-988-142	Sequence 142, App
85	35.5	61.2	307	14	US-10-054-988-142	Sequence 142, App
86	35.5	61.2	307	14	US-10-054-988-142	Sequence 142, App

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OM protein - protein search, using bw model

Run on: March 26, 2005, 10:54:27 ; Search time 17.043 Seconds
(without alignments)
43.800 Million cell updates/sec

Title: US-09-124-280A-31
Perfect score: 58
Sequence: 1 KTCKCKFLKCC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :

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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	10	1	US-08-049-871-2
2	58	100.0	10	1	US-07-813-893-2
3	58	100.0	10	1	US-08-280-397-2
4	58	100.0	10	1	US-08-218-026-49
5	58	100.0	10	2	US-08-653-632-49
6	58	100.0	10	2	US-08-456-112B-31
7	58	100.0	11	1	US-07-813-893-6
8	58	100.0	11	1	US-08-280-397-6
9	58	100.0	11	1	US-08-218-026-50
10	58	100.0	11	2	US-08-653-632-50
11	58	100.0	11	2	US-08-456-112B-35
12	58	100.0	7	1	US-07-813-893-1
13	58	100.0	7	1	US-08-280-397-1
14	58	100.0	7	2	US-08-653-632-1
15	58	100.0	7	2	US-08-456-112B-30
16	58	100.0	7	2	US-08-218-026-49
17	58	100.0	7	2	US-08-653-632-49
18	58	100.0	7	2	US-08-456-112B-31
19	58	100.0	7	2	US-08-280-397-2
20	58	100.0	7	2	US-08-218-026-49
21	58	100.0	7	2	US-08-653-632-49
22	58	100.0	7	2	US-08-456-112B-31
23	58	100.0	7	2	US-08-280-397-2
24	58	100.0	7	2	US-08-218-026-49
25	58	100.0	7	2	US-08-653-632-49
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32	36	62.1	233	4	US-09-270-767-44597	Sequence 44597, A
33	36	62.1	445	4	US-09-167-206-2	Sequence 2, Appl
34	36	62.1	445	4	US-09-538-092-1181	Sequence 1181, Ap
35	36	62.1	490	4	US-09-949-016-7829	Sequence 7829, Ap
36	35.5	61.2	204	4	US-09-904-615-117	Sequence 117, App
37	35.5	61.2	299	4	US-09-904-615-73	Sequence 73, Appl
38	35.5	61.2	307	4	US-09-904-615-142	Sequence 142, App
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Run: March 26, 2005, 12:17:20 ; Search time 30.5215 Seconds

File: 75.937 Million cell updates/sec

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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

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91	91	31	72.1	877	4	US-09-619-353-2	Sequence 2, Appl
92	92	31	72.1	1385	4	US-09-827-998-16	Sequence 16, Appl
93	93	31	72.1	1791	4	US-09-827-998-10	Sequence 10, Appl
94	94	31	72.1	1791	4	US-09-827-998-3	Sequence 3, Appl
95	95	30.5	70.9	12	2	US-08-097-830B-20	Sequence 20, Appl
96	96	30.5	70.9	12	2	US-08-456-1128-20	Sequence 20, Appl
97	97	30	69.8	39	1	US-07-662-225A-4	Sequence 4, Appl
98	98	30	69.8	39	1	US-07-662-225A-5	Sequence 5, Appl
99	99	30	69.8	48	4	US-09-270-767-57331	Sequence 57331, A
100	100	30	69.8	49	1	US-07-662-225A-1	Sequence 18, Appl

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OM protein - protein search, using bw model

March 26, 2005, 12:17:20 ; Search time 47.9624 Seconds
(without alignments)
75.937 Million cell updates/sec

US-09-124-280A-28

Perfect score: 64

Sequence: 1 KRLWKYKXGKF 11

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 33100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications_AA.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	64	100.0	11	9	US-09-124-280A-28
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5	61	95.3	27	14	US-10-131-433-3
6	61	95.3	27	14	US-10-241-173-3
7	61	95.3	101	9	US-09-109-175-5
8	61	95.3	101	9	US-09-109-175-5
9	61	95.3	105	9	US-09-109-175-5
10	61	95.3	105	14	US-10-241-173-2
11	46	71.9	76	15	US-10-424-599-261856
12	46	71.9	222	15	US-10-424-599-220516
13	46	71.9	298	15	US-10-424-599-168507

14	44	68.8	16	14	US-10-271-343-54	Sequence 54, Appl
15	43	67.2	129	15	US-10-264-237-1594	Sequence 1594, Ap
16	43	67.2	237	10	US-09-809-391-418	Sequence 418, App
17	43	67.2	237	10	US-09-882-171-418	Sequence 418, App
18	43	67.2	237	15	US-10-164-861-418	Sequence 418, App
19	43	67.2	297	15	US-10-424-599-275411	Sequence 275411, App
20	43	67.2	652	14	US-10-317-832-107	Sequence 107, App
21	43	67.2	761	14	US-10-317-832-14	Sequence 14, Appl
22	42	65.6	302	15	US-10-424-599-176897	Sequence 176897, Sequence 176897,
23	42	65.6	307	15	US-10-424-599-171211	Sequence 171211,
24	42	65.6	577	15	US-10-104-047-2569	Sequence 2569, Ap
25	42	65.6	661	17	US-10-767-701-1621	Sequence 1621, Ap
26	41	64.1	246	16	US-10-425-114-54991	Sequence 54991, A
27	41	64.1	220	15	US-10-425-114-54991	Sequence 54991, A
28	41	64.1	304	11	US-09-833-245-190	Sequence 190, App
29	41	64.1	338	15	US-10-424-599-259553	Sequence 259553, Sequence 259553,
30	41	64.1	346	15	US-10-424-599-259553	Sequence 131231, Sequence 32465, A
31	41	64.1	1020	16	US-10-437-963-131231	Sequence 57242, A
32	40	62.5	29	14	US-10-029-386-32465	Sequence 145297, Sequence 40924, A
33	40	62.5	93	15	US-10-425-114-57270	Sequence 57270, A
34	40	62.5	125	16	US-10-767-701-57242	Sequence 70295, A
35	40	62.5	273	16	US-10-437-963-145297	Sequence 126874, A
36	40	62.5	291	16	US-10-437-963-145297	Sequence 145297, Sequence 59761, A
37	40	62.5	319	15	US-10-425-114-40924	Sequence 40924, A
38	40	62.5	343	15	US-10-425-114-57270	Sequence 57270, A
39	40	62.5	357	15	US-10-425-114-57270	Sequence 70295, A
40	40	62.5	395	15	US-10-425-114-57270	Sequence 54478, A
41	40	62.5	406	16	US-10-425-114-54478	Sequence 166654, A
42	40	62.5	420	16	US-10-425-114-54478	Sequence 110656, A
43	40	62.5	422	16	US-10-437-963-166654	Sequence 50342, A
44	40	62.5	435	16	US-10-437-963-166654	Sequence 69635, A
45	40	62.5	460	15	US-10-425-114-57270	Sequence 57871, A
46	40	62.5	496	15	US-10-425-114-57871	Sequence 57871, A
47	40	62.5	745	15	US-10-425-114-57871	Sequence 57871, A
48	40	62.5	1446	15	US-10-425-114-57871	Sequence 111298, Sequence 4, Appl1
49	40	62.5	1148	16	US-10-437-963-111298	Sequence 4, Appl1
50	40	62.5	2222	16	US-10-684-141-4	Sequence 3504, Ap
51	40	62.5	2222	17	US-10-810-468-4	Sequence 3504, Ap
52	39	60.9	499	15	US-10-369-493-3504	Sequence 3504, Ap
53	39	60.9	1004	15	US-10-114-270-32	Sequence 38, Appl1
54	39	60.9	2004	14	US-10-331-061-9	Sequence 38, Appl1
55	39	60.9	2029	14	US-10-087-684-38	Sequence 38, Appl1
56	39	60.9	2029	15	US-10-218-779-38	Sequence 39, Appl1
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58	39	60.9	2037	15	US-10-218-779-38	Sequence 153027, Sequence 275441, Sequence 36, Appl1
59	38	59.4	14	16	US-10-469-060-177	Sequence 94, Appl1
60	38	59.4	63	15	US-10-424-599-153027	Sequence 99, Appl1
61	38	59.4	104	15	US-10-424-599-279441	Sequence 1231, App
62	38	59.4	150	14	US-10-138-505-36	Sequence 13375, A
63	38	59.4	150	15	US-10-257-864A-94	Sequence 838, App
64	38	59.4	150	15	US-10-221-111-99	Sequence 153329, Sequence 184005, Sequence 338, App
65	38	59.4	150	15	US-10-321-111-99	Sequence 338, App
66	38	59.4	150	15	US-10-399-518-123	Sequence 338, App
67	38	59.4	216	9	US-09-815-242-13375	Sequence 3049, Ap
68	38	59.4	216	15	US-10-282-122A-73827	Sequence 166, App
69	38	59.4	216	17	US-10-472-928-838	Sequence 522, App
70	38	59.4	245	16	US-10-437-963-151329	Sequence 522, App
71	38	59.4	293	15	US-10-424-599-184005	Sequence 522, App
72	38	59.4	323	17	US-10-363-616-338	Sequence 522, App
73	38	59.4	323	17	US-10-482-029-14	Sequence 522, App
74	38	59.4	353	14	US-10-106-698-6180	Sequence 522, App
75	38	59.4	373	15	US-10-264-049-1049	Sequence 522, App
76	38	59.4	527	9	US-09-962-678-2	Sequence 522, App
77	38	59.4	527	13	US-10-052-866-522	Sequence 522, App
78	38	59.4	527	14	US-10-174-590-522	Sequence 522, App
79	38	59.4	527	14	US-10-174-590-522	Sequence 522, App
80	38	59.4	527	14	US-10-175-737-522	Sequence 522, App
81	38	59.4	527	14	US-10-174-581-522	Sequence 522, App
82	38	59.4	527	14	US-10-176-483-522	Sequence 522, App
83	38	59.4	527	14	US-10-176-483-522	Sequence 522, App
84	38	59.4	527	14	US-10-176-914-522	Sequence 522, App
85	38	59.4	527	14	US-10-176-914-522	Sequence 522, App
86	38	59.4	527	14	US-10-173-706-522	Sequence 522, App

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OM Protein - protein search, using SW model

RunOn: March 26, 2005, 10:54:27 ; Search time 18.7473 Seconds

(without alignments)
43.800 Million cell updates/sec

Title: US-09-124-280a-28

Perfect score: 64
Sequence: 1 KRLKWKYKGF 11Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database:

Issued Patents, AA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	64	100.0	102	2	US-08-760-903-1
6	64	100.0	102	4	US-08-482-191-1
7	64	100.0	102	5	PCT-US96-10237-1
8	61	95.3	19	3	US-08-477-778-15
9	61	95.3	22	3	US-09-160-309-1
10	61	95.3	22	4	US-08-477-778-8
11	61	95.3	22	4	US-09-691-500-1
12	61	95.3	101	1	US-08-264-244-1
13	61	95.3	101	1	US-08-476-688-1
14	61	95.3	101	1	US-08-476-940-1
15	61	95.3	101	1	US-08-704-872-1
16	61	95.3	101	1	US-08-577-464-2
17	61	95.3	101	3	US-08-967-038-1
18	61	95.3	101	3	US-08-871-600A-1
19	61	95.3	105	1	US-08-264-244-3
20	61	95.3	105	1	US-08-476-688-3
21	61	95.3	105	1	US-08-476-940-3
22	61	95.3	105	1	US-08-704-872-3
23	61	95.3	105	3	US-08-967-038-3
24	61	95.3	105	3	US-08-871-600A-3
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26	48	75.0	221	4	US-09-489-039A-13704
27	43	67.2	237	4	US-09-149-476-418

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34	60.9	2004	3	US-09-030-793-9	Sequence 9, Appl
35	60.9	2004	1	US-09-231-899-9	Sequence 9, Appl
36	59.4	78	4	US-09-513-999C-7361	Sequence 7361, Ap
37	59.4	216	4	US-09-583-110-3742	Sequence 4675, Ap
38	59.4	218	4	US-09-107-433-3217	Sequence 3217, Ap
39	59.4	351	4	US-09-949-016-9628	Sequence 3679, Ap
40	57.8	84	4	US-09-134-000C-3655	Sequence 3655, Ap
41	57.8	210	4	US-09-248-796A-15869	Sequence 15869, A
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46	56.2	243	4	US-09-107-532A-6856	Sequence 6856, Ap
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53	54.7	332	1	US-09-347-878-60	Sequence 60, Appl
54	54.7	341	4	US-09-902-540-13885	Sequence 13885, A
55	54.7	393	4	US-09-248-796A-18861	Sequence 18861, A
56	54.7	404	4	US-09-543-681A-4348	Sequence 4348, Ap
57	54.7	737	4	US-09-538-092-921	Sequence 921, Appl
58	54.7	1551	4	US-09-231-899-73	Sequence 73, Appl
59	53.1	25	1	US-07-921-178A-16	Sequence 16, Appl
60	53.1	32	4	US-09-270-767-57653	Sequence 57653, A
61	53.1	51	4	US-09-079-030-84	Sequence 84, Appl
62	53.1	107	3	US-08-654-482-5	Sequence 5, Appl
63	53.1	107	3	US-08-654-482-6	Sequence 6, Appl
64	53.1	108	3	US-08-654-482-1	Sequence 1, Appl
65	53.1	108	3	US-08-654-482-2	Sequence 2, Appl
66	53.1	136	4	US-09-513-999C-5424	Sequence 5424, Ap
67	53.1	139	4	US-09-270-767-40371	Sequence 40371, A
68	53.1	139	4	US-09-270-767-55587	Sequence 55587, A
69	53.1	217	4	US-09-949-016-6509	Sequence 6509, Ap
70	53.1	228	4	US-09-949-016-9719	Sequence 9719, Ap
71	53.1	233	4	US-09-949-016-8117	Sequence 8117, Ap
72	53.1	249	4	US-09-252-991A-16620	Sequence 16620, A
73	53.1	259	4	US-09-328-352-7755	Sequence 7755, Ap
74	53.1	261	3	US-09-489-039A-7997	Sequence 7997, Ap
75	53.1	290	3	US-09-134-001C-4044	Sequence 4044, Ap
76	53.1	292	4	US-09-902-540-15020	Sequence 15020, A
77	53.1	367	3	US-09-166-205B-68	Sequence 68, Appl
78	53.1	367	4	US-09-806-658-4	Sequence 4, Appl
79	53.1	372	2	US-08-501-003A-12	Sequence 12, Appl
80	53.1	379	4	US-09-079-030-81	Sequence 81, Appl
81	53.1	383	2	US-08-501-003A-14	Sequence 14, Appl
82	53.1	389	2	US-08-501-003A-11	Sequence 11, Appl
83	53.1	391	1	US-07-921-178A-2	Sequence 2, Appl
84	53.1	391	1	US-08-103-445-5	Sequence 5, Appl
85	53.1	391	1	US-08-461-690B-5	Sequence 5, Appl
86	53.1	391	2	US-08-501-003A-13	Sequence 13, Appl
87	53.1	391	2	US-08-501-003A-16	Sequence 16, Appl
88	53.1	391	4	US-09-275-252A-13	Sequence 5304, Ap
89	53.1	391	4	US-09-949-016-5904	Sequence 29, Appl
90	53.1	393	3	US-09-230-771A-29	Sequence 22719, A
91	53.1	397	4	US-09-252-991A-12719	Sequence 15, Appl
92	53.1	398	2	US-08-501-003A-15	Sequence 15, Appl
93	53.1	411	4	US-09-949-016-8100	Sequence 8100, Ap
94	53.1	425	3	US-09-230-771A-30	Sequence 30, Appl
95	53.1	439	4	US-09-949-016-11463	Sequence 11463, A
96	53.1	450	2	US-08-611-280-2	Sequence 2, Appl
97	53.1	450	2	US-08-611-280-25	Sequence 25, Appl
98	53.1	450	3	US-09-195-940-2	Sequence 25, Appl
99	53.1	450	3	US-09-195-940-25	Sequence 25, Appl
100	53.1	450	3	US-09-362-466-2	Sequence 2, Appl

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OM protein - protein search, using sw model

RunOn: March 26, 2005, 12:17:20 ; Search time 43.6021 Seconds

744 (without alignments)
75.937 Million cell updates/sec

Title: US-09-124-280A-27

Percent score: 55

Sequence: 1 KMAQKRFLEK 10

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	10	9	US-09-765-527-8
2	55	100.0	10	9	US-09-124-280A-27
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4	55	100.0	10	15	US-10-446-628-8
5	55	100.0	10	15	US-10-319-786-8
6	55	100.0	12	9	US-09-765-527-125
7	55	100.0	13	14	US-10-131-686A-30
8	55	100.0	14	9	US-09-765-527-123
9	55	100.0	14	14	US-10-131-686A-37
10	55	100.0	14	15	US-10-446-628-164
11	55	100.0	15	9	US-09-765-527-2
12	55	100.0	15	9	US-09-765-527-9
13	55	100.0	15	9	US-09-765-527-16

14	55	100.0	15	9	US-09-765-527-17	Sequence 17, Appl
15	55	100.0	15	9	US-09-765-527-18	Sequence 18, Appl
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OM: protein - protein search, using SW model

Run on: March 26, 2005, 10:54:27 ; Search time 17.043 Seconds

(without alignments)
43.800 Million cell updates/sec

US-09-124-280a-27

Perfect score: 55

Sequence: 1 KMKAKRPLK 10

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8	55	100.0	10 1 US-08-218-026-6	Sequence 6, Appli
9	55	100.0	10 2 US-08-653-632-6	Sequence 6, Appli
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CM Protein - protein search, using SW model

Run on: March 26, 2005, 12:17:20 ; Search time 39.2419 Seconds

(without alignments)
75.937 Million cell updates/sec

US-09-124-280a-26

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Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1407402 seqs, 33100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database:

Published Applications: AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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81	50	100.0	27	US-10-300-608-31	Sequence 31, Appl
82	50	100.0	27	US-10-446-628-11	Sequence 11, Appl
83	50	100.0	27	US-10-319-786-11	Sequence 11, Appl
84	50	100.0	29	US-09-765-527-64	Sequence 64, Appl
85	50	100.0	29	US-10-446-628-53	Sequence 53, Appl
86	50	100.0	29	US-10-319-786-53	Sequence 53, Appl

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OM,protein - protein search, using sw model

Run on: March 26, 2005, 10:54:27 ; Search time 15.3387 Seconds
(without alignments)
43.800 Million cell updates/sec

US-09-124-280a-26

Sequence: 1 KMKAKRFL 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	50	100.0	10	1	US-08-372-783-8
5	50	100.0	10	1	US-08-372-783-8
6	50	100.0	10	1	US-08-097-830E-27
7	50	100.0	10	1	US-08-306-473A-8
8	50	100.0	10	1	US-08-209-762-8
9	50	100.0	10	1	US-08-473-344-8
10	50	100.0	10	1	US-08-218-026-6
11	50	100.0	10	2	US-08-653-632-6
12	50	100.0	10	2	US-08-456-112B-27
13	50	100.0	10	2	US-08-621-803-8
14	50	100.0	10	2	US-08-485-445A-8
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16	50	100.0	10	3	US-09-119-263-8
17	50	100.0	10	3	US-08-657-162-8
18	50	100.0	10	3	US-09-224-480-8
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24	50	100.0	10	5	PCT-US95-00498-8
25	50	100.0	10	5	PCT-US95-00656-8
26	50	100.0	11	1	US-08-218-026-7
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29	50	100.0	11	2	US-08-653-632-26	Sequence 26, Appl
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62	50	100.0	14	2	US-08-621-803-123	Sequence 123, App
63	50	100.0	14	2	US-08-485-445A-164	Sequence 164, App
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65	50	100.0	14	3	US-08-657-162-164	Sequence 164, App
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68	50	100.0	14	3	US-09-280-909A-37	Sequence 37, Appl
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71	50	100.0	14	4	PCT-US94-06931-37	Sequence 37, App
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OM protein - protein search, using SW model

Run On: March 26, 2005, 12:17:20 ; Search time 34.8817 Seconds

(without alignments)
75.937 Million cell updates/sec

US-09-124-280A-25

Perfect score: 37

Sequence: 1 KELLRIKI 8

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1407402 seqs, 33110923 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications AA*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	37	100.0	22	US-10-446-628-3	Sequence 3, Appl
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8	37	100.0	29	US-10-446-628-1	Sequence 1, Appl
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15	37	100.0	198	US-10-131-686A-56	Sequence 56, Appl
16	37	100.0	199	US-10-131-686A-47	Sequence 47, Appl
17	37	100.0	199	US-10-131-686A-54	Sequence 54, Appl
18	37	100.0	199	US-10-131-686A-57	Sequence 57, Appl
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56	37	100.0	487	US-10-359-013-13	Sequence 13, Appl
57	37	100.0	63	US-10-424-599-272164	Sequence 272164, Appl
58	37	89.2	15	US-09-765-527-1	Sequence 1, Appl
59	37	89.2	15	US-10-446-628-4	Sequence 4, Appl
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63	37	89.2	125	US-10-437-963-108319	Sequence 108319, Appl
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OMP:protein - protein search, using sw model

March 26, 2005, 10:54:27 : Search time 13.6344 Seconds
(without alignments)
43.800 Million cell updates/sec

US-09-124-280a-25

Seq. ID: 37

Seq. Index: 1 KEXRIKI 8

Score: 10.0, Gapext 0.5

Search: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

Result No.	Score	Query Length	ID	Description
1	37 100.0	8 1	US-08-097-830E-25	Sequence 25, Appl
2	37 100.0	8 2	US-08-456-112B-25	Sequence 25, Appl
3	37 100.0	11 1	US-08-218-026-14	Sequence 14, Appl
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9	37 100.0	15 1	US-08-372-105-5	Sequence 5, Appl
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11	37 100.0	15 1	US-08-209-762-5	Sequence 5, Appl
12	37 100.0	15 1	US-08-473-344-5	Sequence 5, Appl
13	37 100.0	15 2	US-08-621-803-55	Sequence 55, Appl
14	37 100.0	15 2	US-08-485-445A-5	Sequence 5, Appl
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Runfile: March 26, 2005, 12:17:20 / Search time 39.2419 Seconds
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Pred. No. is the number of results predicted by chance to have a
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March 26, 2005, 10:54:27 ; Search time 15.3387 Seconds
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US-09-124-280A-24

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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Listing first 1000 summaries

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OM protein - protein search, using SW model

Run on: March 26, 2005, 10:43:56 ; Search time 47.3936 Seconds

(without alignments)
76.848 Million cell updates/sec

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Gapop 10.0, Gapext 0.5

Sequences: 1407402 seqs, 31100923 residues

Maximum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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55	32	61.5	880	14	US-10-032-585-1525	Sequence 7525, Ap
56	32	61.5	892	15	US-10-369-493-22811	Sequence 22811, A
57	32	61.5	911	15	US-10-369-493-12464	Sequence 12464, A
58	32	61.5	936	16	US-10-408-765A-1935	Sequence 1935, Ap
59	32	61.5	1028	15	US-10-369-493-3464	Sequence 3464, Ap
60	32	61.5	1153	15	US-10-282-122A-52674	Sequence 52674, A
61	32	61.5	1251	16	US-10-437-963-161694	Sequence 161694,
62	32	61.5	1401	16	US-10-437-963-175375	Sequence 175375,
63	32	61.5	1722	14	US-10-141-956-1	Sequence 1, Appl
64	32	61.5	1722	14	US-10-207-655-145	Sequence 145, App
65	32	61.5	1953	15	US-10-369-493-1945	Sequence 1945, Ap
66	32	61.5	2351	16	US-10-437-963-170608	Sequence 170608,
67	32	61.5	4753	15	US-10-369-493-5119	Sequence 5119, Ap
68	31	59.6	689	15	US-10-369-493-2534	Sequence 2534, Ap
69	31	59.6	81	15	US-10-424-599-285238	Sequence 285238,
70	31	59.6	30	15	US-10-424-599-180208	Sequence 180208,
71	31	59.6	52	14	US-10-218-102-354	Sequence 354, App
72	31	59.6	74	15	US-10-424-599-188575	Sequence 188575,
73	31	59.6	78	14	US-10-023-896-120	Sequence 120, App
74	31	59.6	81	14	US-10-023-896-119	Sequence 119, App
75	31	59.6	82	9	US-09-867-550-492	Sequence 492, App
76	31	59.6	109	15	US-10-282-122A-47531	Sequence 47531, A
77	31	59.6	109	15	US-10-282-122A-49015	Sequence 49015, A
78	31	59.6	109	15	US-10-282-122A-50330	Sequence 50330, A
79	31	59.6	109	16	US-10-437-963-115311	Sequence 115311,
80	31	59.6	117	14	US-10-023-896-57	Sequence 57, Appl
81	31	59.6	117	16	US-10-767-701-62867	Sequence 62867, A
82	31	59.6	130	15	US-10-424-599-275308	Sequence 275308,
83	31	59.6	133	15	US-10-264-049-2270	Sequence 2270, Ap
84	31	59.6	147	15	US-10-424-599-182233	Sequence 182233,
85	31	59.6	155	16	US-10-767-701-55568	Sequence 55568, A
86	31	59.6	173	15	US-10-335-977-8773	Sequence 8773, Ap

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OM protein - protein search, using ew model

Run on: March 26, 2005, 10:25:00 / Search time 18.5479 Seconds
(without alignments)
44.271 Million cell updates/sec

Target: US-09-124-280A-22

Perfect score: 52

Sequence: 1 KSLUKRUTR 11

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database: Issued Patents AA.*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	52	100.0	11	1	US-08-097-830E-22
2	52	100.0	11	2	US-08-456-112B-22
3	44	84.6	366	3	US-08-746-883-6
4	44	84.6	366	4	US-09-313-117-6
5	35	67.3	62	4	US-09-489-039A-13884
6	34	65.4	123	4	US-09-270-767-35521
7	34	65.4	123	4	US-09-270-767-50738
8	34	65.4	322	4	US-09-252-991A-28933
9	34	65.4	439	4	US-09-252-991A-28709
10	33	63.5	444	4	US-09-591-466C-6
11	33	63.5	542	4	US-09-252-991A-29987
12	32	61.5	126	4	US-09-732-210-1163
13	32	61.5	324	4	US-09-248-796A-16351
14	32	61.5	355	4	US-09-270-767-36315
15	32	61.5	355	4	US-09-270-767-51532
16	32	61.5	431	4	US-09-592-998C-9
17	32	61.5	435	4	US-09-592-998C-10
18	32	61.5	487	4	US-09-328-352-6206
19	32	61.5	495	4	US-09-248-796A-20007
20	32	61.5	598	4	US-09-650-334A-58
21	32	61.5	751	4	US-09-540-236-2921
22	32	61.5	1722	4	US-09-194-612A-1
23	31	59.6	50	4	US-09-621-976-5023
24	31	59.6	115	4	US-09-345-236B-131
25	31	59.6	148	4	US-09-328-352-8000
26	31	59.6	154	4	US-09-252-991A-31799
27	31	59.6	163	4	US-09-270-767-36854

28	31	59.6	163	4	US-09-270-767-52071	Sequence 52071, A
29	31	59.6	179	4	US-09-252-991A-30388	Sequence 30388, A
30	31	59.6	241	2	US-08-865-273-2	Sequence 2, Appl1
31	31	59.6	241	3	US-09-385-174-2	Sequence 2, Appl1
32	31	59.6	333	4	US-09-248-796A-20704	Sequence 20704, A
33	31	59.6	420	2	US-08-588-258B-40	Sequence 40, Appl1
34	31	59.6	420	5	PCT-US96-08295-40	Sequence 40, Appl1
35	31	59.6	428	3	US-09-108-020-2	Sequence 2, Appl1
36	31	59.6	428	3	US-09-108-020-33	Sequence 33, Appl1
37	31	59.6	428	3	US-09-685-296-2	Sequence 2, Appl1
38	31	59.6	428	4	US-09-685-296-33	Sequence 33, Appl1
39	31	59.6	439	3	US-09-457-045B-68	Sequence 68, Appl1
40	31	59.6	439	4	US-09-866-570B-68	Sequence 68, Appl1
41	31	59.6	552	4	US-08-675-499A-2	Sequence 2, Appl1
42	31	59.6	552	4	US-08-812-008-2	Sequence 2, Appl1
43	31	59.6	552	4	US-09-949-016-6608	Sequence 6608, Ap
44	31	59.6	609	4	US-09-902-540-12674	Sequence 12674, A
45	31	59.6	844	4	US-09-949-016-9438	Sequence 9438, Ap
46	31	59.6	1038	4	US-09-538-092-487	Sequence 487, Ap
47	31	59.6	1248	3	US-08-726-214-16	Sequence 16, Appl
48	30	57.7	121	4	US-09-543-681A-7237	Sequence 7237, Ap
49	30	57.7	147	4	US-09-732-210-1347	Sequence 1347, Ap
50	30	57.7	162	4	US-09-270-767-38772	Sequence 38772, A
51	30	57.7	162	4	US-09-270-767-53989	Sequence 53989, A
52	30	57.7	179	3	US-09-134-001C-3711	Sequence 3711, Ap
53	30	57.7	233	4	US-09-248-796A-19554	Sequence 19554, A
54	30	57.7	256	4	US-09-583-110-4113	Sequence 4113, Ap
55	30	57.7	260	3	US-09-134-001C-4507	Sequence 4507, Ap
56	30	57.7	266	4	US-09-252-991A-19949	Sequence 19949, A
57	30	57.7	280	4	US-09-489-039A-10103	Sequence 10103, A
58	30	57.7	294	4	US-09-107-532A-5153	Sequence 5153, Ap
59	30	57.7	294	4	US-09-134-000C-6529	Sequence 6529, Ap
60	30	57.7	305	4	US-09-270-767-60012	Sequence 60012, A
61	30	57.7	311	4	US-09-543-681A-4963	Sequence 4963, Ap
62	30	57.7	311	4	US-09-489-039A-9759	Sequence 9759, Ap
63	30	57.7	346	4	US-09-328-352-7531	Sequence 7531, Ap
64	30	57.7	357	4	US-09-107-433-3434	Sequence 3434, Ap
65	30	57.7	398	4	US-09-543-681A-5007	Sequence 5007, Ap
66	30	57.7	411	4	US-09-270-767-45780	Sequence 45780, A
67	30	57.7	440	4	US-09-270-767-44562	Sequence 44562, A
68	30	57.7	456	3	US-08-858-207A-366	Sequence 366, App
69	30	57.7	459	4	US-09-248-796A-20540	Sequence 20540, A
70	30	57.7	508	4	US-09-489-039A-7307	Sequence 7307, Ap
71	30	57.7	575	4	US-09-248-796A-15765	Sequence 15765, A
72	30	57.7	619	4	US-09-540-236-2182	Sequence 2182, Ap
73	30	57.7	626	4	US-09-252-991A-20268	Sequence 20268, A
74	30	57.7	626	4	US-09-489-039A-13685	Sequence 13685, A
75	30	57.7	749	4	US-09-583-110-2921	Sequence 2921, Ap
76	30	57.7	806	4	US-09-107-433-2944	Sequence 2944, Ap
77	30	57.7	849	4	US-09-538-092-54	Sequence 54, Appl
78	30	57.7	951	4	US-09-248-796A-20520	Sequence 20520, A
79	30	57.7	1010	4	US-09-654-449-2	Sequence 2, Appl1
80	30	57.7	1010	4	US-09-759-152A-2	Sequence 2, Appl1
81	30	57.7	1031	4	US-09-489-039A-11186	Sequence 11186, A
82	30	57.7	1121	1	US-07-789-915A-2	Sequence 2, Appl1
83	30	57.7	1121	1	US-08-005-002C-2	Sequence 2, Appl1
84	30	57.7	1221	1	US-08-487-203A-2	Sequence 2, Appl1
85	30	57.7	1403	1	US-07-908-253-3	Sequence 3, Appl1
86	30	57.7	1403	2	US-08-694-865-17	Sequence 17, Appl1
87	30	57.7	1403	2	US-08-535-837-3	Sequence 3, Appl1
88	30	57.7	1403	3	US-09-124-491-17	Sequence 17, Appl1
89	30	57.7	1403	3	US-09-383-912-17	Sequence 17, Appl1
90	30	57.7	1618	1	US-07-853-913-4	Sequence 4, Appl1
91	30	57.7	1618	1	US-09-538-092-1133	Sequence 1133, Ap
92	30	57.7	1805	1	US-07-853-913-2	Sequence 2, Appl1
93	29	55.8	405	4	US-09-270-767-56734	Sequence 56734, A
94	29	55.8	52	4	US-09-513-999C-5120	Sequence 5120, Ap
95	29	55.8	82	4	US-09-252-991A-32127	Sequence 32127, A
96	29	55.8	109	4	US-09-248-796A-22722	Sequence 22722, A
97	29	55.8	127	4	US-09-621-976-4370	Sequence 4370, Ap
98	29	55.8	128	4	US-09-660-107-4	Sequence 4, Appl1
99	29	55.8	129	4	US-09-549-519-37	Sequence 37, Appl1
100	29	55.8	129	4	US-09-549-519-38	Sequence 38, Appl1

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OM protein - protein search, using SW model

Run on: March 26, 2005, 10:43:56 ; Search time 38.7766 Seconds
(without alignments)
76.848 Million cell updates/sec

Title: US-09-124-280a-21

Perfect score: 40

Sequence: 1 VKALVRRL 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Search: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA.*

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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	40	100.0	375	US-10-207-655-178	Sequence 178, Appl
6	40	100.0	375	US-10-331-496a-23	Sequence 23, Appl
7	40	100.0	431	US-09-925-302-485	Sequence 485, Appl
8	40	100.0	431	US-09-925-302-485	Sequence 485, Appl
9	34	85.0	1229	US-10-437-963-133251	Sequence 133251, Appl
10	33	82.5	269	US-10-424-599-193020	Sequence 193020, Appl
11	33	82.5	842	US-10-437-963-111774	Sequence 111774, Appl
12	33	82.5	1857	US-10-437-963-152007	Sequence 152007, Appl
13	32	80.0	20	US-10-340-288-30	Sequence 30, Appl

14	32	80.0	193	US-09-862-540-45	Sequence 45, Appl
15	32	80.0	206	US-10-369-493-19930	Sequence 19930, A
16	32	80.0	218	US-10-369-493-2768	Sequence 2768, Ap
17	32	80.0	224	US-09-764-864-1465	Sequence 1465, Ap
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24	31	77.5	208	US-10-369-493-19007	Sequence 19007, A
25	31	77.5	222	US-10-156-761-11707	Sequence 11707, A
26	31	77.5	263	US-10-264-049-2406	Sequence 2406, Ap
27	31	77.5	329	US-10-287-226-294	Sequence 226, App
28	31	77.5	367	US-10-425-114-48334	Sequence 48334, A
29	31	77.5	416	US-10-437-963-113397	Sequence 113397, A
30	31	77.5	444	US-10-437-963-194130	Sequence 194130, A
31	31	77.5	492	US-10-282-122a-44750	Sequence 44750, A
32	31	77.5	549	US-10-220-120-219	Sequence 219, App
33	31	77.5	785	US-10-437-963-139958	Sequence 139958, A
34	31	77.5	949	US-10-437-963-184048	Sequence 184048, A
35	30	75.0	159	US-10-425-114-53858	Sequence 53858, A
36	30	75.0	168	US-10-767-761-44894	Sequence 44894, A
37	30	75.0	172	US-10-437-963-167849	Sequence 167849, A
38	30	75.0	249	US-10-369-493-4789	Sequence 4789, Ap
39	30	75.0	259	US-10-369-493-7549	Sequence 7549, Ap
40	30	75.0	416	US-10-389-647-630	Sequence 630, App
41	30	75.0	433	US-10-425-114-4439	Sequence 4439, A
42	30	75.0	437	US-10-437-963-134689	Sequence 134689, A
43	30	75.0	479	US-10-437-963-105375	Sequence 105375, A
44	30	75.0	485	US-10-282-122a-52587	Sequence 52587, A
45	30	75.0	990	US-09-764-875-774	Sequence 774, App
46	30	75.0	1101	US-10-437-963-106991	Sequence 106991, A
47	30	75.0	1459	US-10-408-765a-2246	Sequence 2246, Ap
48	30	75.0	1681	US-10-398-885a-16	Sequence 16, Appl
49	29	72.5	64	US-10-424-599-237181	Sequence 237181, A
50	29	72.5	74	US-10-767-701-53660	Sequence 53660, A
51	29	72.5	115	US-10-424-599-158077	Sequence 158077, A
52	29	72.5	120	US-10-425-114-70083	Sequence 70083, A
53	29	72.5	138	US-10-424-599-272544	Sequence 272544, A
54	29	72.5	174	US-09-927-602-11	Sequence 11, Appl
55	29	72.5	180	US-10-767-701-60307	Sequence 60307, A
56	29	72.5	193	US-10-437-963-169782	Sequence 169782, A
57	29	72.5	213	US-10-424-599-158076	Sequence 158076, A
58	29	72.5	298	US-10-282-122a-65140	Sequence 65140, A
59	29	72.5	326	US-10-282-122a-66105	Sequence 66105, A
60	29	72.5	329	US-10-437-963-151899	Sequence 151899, A
61	29	72.5	376	US-10-437-963-122802	Sequence 122802, A
62	29	72.5	401	US-10-282-122a-47914	Sequence 47914, A
63	29	72.5	435	US-09-825-751a-14	Sequence 14, Appl
64	29	72.5	479	US-10-087-192-126	Sequence 126, App
65	29	72.5	481	US-10-087-192-123	Sequence 123, App
66	29	72.5	483	US-10-282-122a-67576	Sequence 67576, A
67	29	72.5	486	US-10-282-122a-43117	Sequence 43117, A
68	29	72.5	490	US-10-437-963-128517	Sequence 128517, A
69	29	72.5	496	US-10-437-963-182682	Sequence 182682, A
70	29	72.5	524	US-10-369-493-8241	Sequence 8241, Ap
71	29	72.5	549	US-10-437-963-179210	Sequence 179210, A
72	29	72.5	567	US-09-815-342-11885	Sequence 11885, A
73	29	72.5	567	US-10-282-122a-66420	Sequence 66420, A
74	29	72.5	570	US-10-437-963-186759	Sequence 186759, A
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76	29	72.5	581	US-10-282-122a-66524	Sequence 66524, A
77	29	72.5	598	US-10-437-963-138174	Sequence 138174, A
78	29	72.5	603	US-10-437-963-169783	Sequence 169783, A
79	29	72.5	633	US-10-282-122a-54071	Sequence 54071, A
80	29	72.5	650	US-10-437-963-128508	Sequence 128508, A
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82	29	72.5	735	US-10-282-122a-61204	Sequence 61204, A
83	29	72.5	756	US-10-437-963-175575	Sequence 175575, A
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85	29	72.5	1040	US-10-437-963-162180	Sequence 162180, A
86	29	72.5	1047	US-10-437-963-138135	Sequence 138135, A

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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:25:00 ; Search time 15.1755 Seconds
(without alignments)
44.271 Million cell updates/sec

Database: US-09-124-280A-21

Perfect score: 40

Sequence: 1 VKALRVRL 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Search: 513545 seqs, 74649064 residues

Typical number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	40	100.0	9	2	US-08-456-112B-21
3	40	100.0	138	2	US-08-484-397A-15
4	40	100.0	152	2	US-08-484-397A-9
5	40	100.0	152	2	US-08-484-397A-10
6	40	100.0	152	2	US-08-484-397A-11
7	40	100.0	152	2	US-08-484-397A-12
8	40	100.0	152	2	US-08-484-397A-13
9	40	100.0	152	2	US-08-484-397A-14
10	40	100.0	334	1	US-08-484-397A-8
11	40	100.0	348	1	US-08-366-953A-45
12	40	100.0	348	2	US-08-484-397A-2
13	40	100.0	348	2	US-08-484-397A-3
14	40	100.0	348	2	US-08-484-397A-4
15	40	100.0	348	2	US-08-484-397A-5
16	40	100.0	348	2	US-08-484-397A-6
17	40	100.0	348	2	US-08-484-397A-7
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19	40	100.0	348	2	US-08-484-397A-38
20	40	100.0	375	1	US-08-205-719-2
21	40	100.0	375	3	US-08-746-883-5
22	40	100.0	375	4	US-09-313-177-5
23	39	97.5	373	3	US-08-746-883-4
24	39	97.5	373	4	US-09-313-177-4
25	34	85.0	125	4	US-09-252-991A-25564
26	33	82.5	193	4	US-09-252-991A-28415
27	33	82.5	461	1	US-07-796-361A-13

28	33	82.5	462	1	US-07-612-673-4	Sequence 4, Appl1
29	33	82.5	462	1	US-08-539-666-4	Sequence 4, Appl1
30	33	82.5	1219	4	US-09-252-991A-28840	Sequence 28840, A
31	32	80.0	777	4	US-09-949-016-7158	Sequence 7158, Ap
32	32	80.0	1439	2	US-08-449-644-2	Sequence 2, Appl1
33	32	80.0	1439	2	US-08-087-244A-2	Sequence 2, Appl1
34	32	80.0	1439	2	US-08-652-971-3	Sequence 3, Appl1
35	32	80.0	1457	2	US-08-449-644-1	Sequence 1, Appl1
36	32	80.0	1457	2	US-08-087-244A-1	Sequence 1, Appl1
37	32	80.0	1457	2	US-08-991-258A-3	Sequence 3, Appl1
38	32	80.0	1457	2	US-08-769-399-3	Sequence 3, Appl1
39	32	80.0	1457	3	US-08-991-953A-3	Sequence 3, Appl1
40	31	77.5	511	4	US-09-328-352-5220	Sequence 5220, Ap
41	30	75.0	403	3	US-08-822-774-19	Sequence 19, Appl1
42	30	75.0	403	3	US-09-632-711-19	Sequence 19, Appl1
43	30	75.0	403	3	US-09-632-703B-19	Sequence 19, Appl1
44	30	75.0	403	4	US-09-632-702-19	Sequence 19, Appl1
45	30	75.0	403	4	US-09-399-003-19	Sequence 19, Appl1
46	30	75.0	517	4	US-09-352-991A-32044	Sequence 32044, A
47	30	75.0	558	4	US-09-902-540-11142	Sequence 11142, A
48	30	75.0	1246	4	US-09-252-991A-23140	Sequence 23140, A
49	30	75.0	1676	4	US-09-949-016-7610	Sequence 7610, Ap
50	30	75.0	2958	3	US-08-894-344C-2	Sequence 2, Appl1
51	29	72.5	62	4	US-09-621-976-7602	Sequence 7602, Ap
52	29	72.5	84	4	US-09-513-999C-8596	Sequence 5596, Ap
53	29	72.5	256	4	US-09-270-767-35216	Sequence 35216, A
54	29	72.5	256	4	US-09-270-767-50433	Sequence 50433, A
55	29	72.5	338	4	US-09-902-540-16254	Sequence 16254, A
56	29	72.5	343	4	US-09-252-991A-19553	Sequence 19553, A
57	29	72.5	466	4	US-09-252-991A-31929	Sequence 31929, A
58	29	72.5	479	2	US-08-899-514-2	Sequence 2, Appl1
59	29	72.5	508	4	US-09-902-540-12025	Sequence 12025, A
60	29	72.5	559	4	US-09-252-991A-30324	Sequence 30324, A
61	29	72.5	594	4	US-09-252-991A-26272	Sequence 26272, A
62	29	72.5	620	4	US-09-252-991A-21110	Sequence 21110, A
63	29	72.5	866	4	US-09-902-540-15310	Sequence 15310, A
64	28	70.0	136	4	US-09-252-991A-18112	Sequence 18112, A
65	28	70.0	142	4	US-09-252-991A-18333	Sequence 18333, A
66	28	70.0	191	4	US-09-270-767-32828	Sequence 32828, A
67	28	70.0	142	4	US-09-248-796A-16998	Sequence 16998, A
68	28	70.0	292	4	US-09-270-767-33808	Sequence 33808, A
69	28	70.0	297	4	US-09-248-796A-25364	Sequence 25364, A
70	28	70.0	299	4	US-10-311-582-2	Sequence 2, Appl1
71	28	70.0	312	4	US-09-252-991A-28383	Sequence 28383, A
72	28	70.0	312	4	US-09-902-540-16271	Sequence 16271, A
73	28	70.0	397	4	US-09-252-991A-30059	Sequence 30059, A
74	28	70.0	467	3	US-09-306-595C-6	Sequence 6, Appl1
75	28	70.0	467	4	US-09-925-188-6	Sequence 23374, A
76	28	70.0	504	4	US-09-352-991A-23374	Sequence 5774, Ap
77	28	70.0	514	4	US-09-134-000C-5774	Sequence 31236, A
78	28	70.0	516	4	US-09-252-991A-15128	Sequence 15128, A
79	28	70.0	566	4	US-09-902-540-15162	Sequence 15162, A
80	28	70.0	665	4	US-09-543-681A-7757	Sequence 7757, Ap
81	28	70.0	756	4	US-09-919-497-66	Sequence 66, Appl1
82	28	70.0	764	4	US-09-902-540-14495	Sequence 14495, A
83	28	70.0	776	4	US-09-949-016-7231	Sequence 7231, Ap
84	28	70.0	808	4	US-09-270-767-62346	Sequence 62346, A
85	28	70.0	1019	4	US-09-434-066-23	Sequence 23, Appl1
86	28	70.0	1086	4	US-09-252-991A-20186	Sequence 20186, A
87	28	70.0	1333	4	US-09-370-767-46728	Sequence 46728, A
88	28	70.0	1653	4	US-09-107-433-4155	Sequence 4155, Ap
89	28	70.0	2257	4	US-09-339-477-8	Sequence 8, Appl1
90	28	70.0	2867	4	US-09-902-540-12593	Sequence 12593, A
91	27	67.5	60	4	US-09-732-210-879	Sequence 879, Ap
92	27	67.5	72	4	US-09-621-976-6257	Sequence 6257, Ap
93	27	67.5	77	4	US-09-248-796A-26197	Sequence 26197, A
94	27	67.5	81	1	US-08-259-672-8	Sequence 8, Appl1
95	27	67.5	81	1	US-08-459-351-8	Sequence 8, Appl1
96	27	67.5	81	1	US-08-460-533-8	Sequence 8, Appl1
97	27	67.5	81	5	PCT-US94-06654-8	Sequence 8, Appl1
98	27	67.5	99	1	US-08-259-672-7	Sequence 7, Appl1
99	27	67.5	99	1	US-08-459-351-7	Sequence 7, Appl1
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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:43:56 ; Search time 43.0851 Seconds
(without alignments)
76.848 Million cell updates/sec

Title: US-09-124-280A-19
Perfect score: 62
Sequence: 1 CCKKKFFFC 10

Scoring table: BIOSUN62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 311100923 residues
Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	50	80.6	93	15	US-10-424-599-232634
3	48	77.4	120	15	US-10-424-599-270923
4	44	71.0	23	15	US-10-176-419A-2
5	44	71.0	67	16	US-10-437-963-192982
6	44	71.0	121	16	US-10-437-963-116634
7	44	71.0	128	16	US-10-437-963-189194
8	42	67.7	48	15	US-10-424-599-251375
9	42	67.7	72	16	US-10-437-963-190801
10	42	67.7	91	15	US-10-424-599-252891
11	42	67.7	136	15	US-10-424-599-254075
12	41	66.1	64	15	US-10-424-599-252365
13	41	66.1	71	15	US-10-424-599-245989

14	41	66.1	73	15	US-10-424-599-209175	Sequence 209175,
15	41	66.1	90	15	US-10-424-599-166534	Sequence 166534,
16	41	66.1	293	16	US-10-451-467A-524	Sequence 524, App
17	41	66.1	293	17	US-10-741-849-7156	Sequence 7156, Ap
18	41	66.1	352	8	US-08-979-847-1118	Sequence 118, App
19	41	66.1	352	14	US-10-114-104-1118	Sequence 118, App
20	41	66.1	363	15	US-10-632-793-11	Sequence 31, App1
21	41	66.1	378	8	US-08-979-847-1122	Sequence 122, App
22	41	66.1	378	14	US-10-114-104-122	Sequence 122, App
23	41	66.1	393	15	US-10-632-793-11	Sequence 11, App1
24	41	66.1	398	8	US-08-979-847-1121	Sequence 121, App
25	41	66.1	398	14	US-10-114-104-121	Sequence 121, App
26	41	66.1	409	15	US-10-632-793-10	Sequence 15, App1
27	41	66.1	420	15	US-10-637-565-15	Sequence 15, App1
28	41	66.1	926	16	US-10-437-963-179451	Sequence 179451,
29	40	64.5	45	16	US-10-437-963-139479	Sequence 139479,
30	40	64.5	52	15	US-10-424-599-264645	Sequence 264645,
31	40	64.5	113	15	US-09-374-046A-146	Sequence 146, App
32	40	64.5	113	15	US-10-616-263-146	Sequence 146, App
33	40	64.5	488	16	US-10-437-963-163387	Sequence 163387,
34	40	64.5	490	16	US-10-767-701-45642	Sequence 45642, A
35	39.5	63.7	135	15	US-10-424-599-204785	Sequence 204785,
36	39	62.9	18	10	US-09-747-802-65	Sequence 65, App1
37	39	62.9	18	10	US-09-865-294-58	Sequence 65, App1
38	39	62.9	18	16	US-10-789-619-65	Sequence 187048,
39	39	62.9	44	15	US-10-424-599-187048	Sequence 271690,
40	39	62.9	47	15	US-10-424-599-271690	Sequence 246406,
41	39	62.9	51	15	US-10-424-599-246406	Sequence 271256,
42	39	62.9	51	15	US-10-424-599-271256	Sequence 161136,
43	39	62.9	56	15	US-10-424-599-161136	Sequence 227695,
44	39	62.9	56	15	US-10-424-599-227695	Sequence 236855,
45	39	62.9	57	15	US-10-424-599-236855	Sequence 179026,
46	39	62.9	62	16	US-10-437-963-176026	Sequence 104, App
47	39	62.9	86	15	US-09-895-298-104	Sequence 149695,
48	39	62.9	86	15	US-10-424-599-149695	Sequence 205963,
49	39	62.9	90	15	US-10-424-599-205963	Sequence 221788,
50	39	62.9	91	15	US-10-424-599-221788	Sequence 176698,
51	39	62.9	102	15	US-10-424-599-176698	Sequence 134472,
52	39	62.9	110	16	US-10-437-963-134472	Sequence 193220,
53	39	62.9	114	15	US-10-424-599-193220	Sequence 153560,
54	39	62.9	134	15	US-10-424-599-153560	Sequence 908, App
55	39	62.9	162	15	US-10-412-699B-908	Sequence 3, App1
56	38	61.3	29	11	US-09-725-945-3	Sequence 472651, A
57	38	61.3	45	16	US-10-767-701-472651	Sequence 232651,
58	38	61.3	50	15	US-10-424-599-232651	Sequence 196936,
59	38	61.3	54	15	US-10-424-599-196936	Sequence 163741,
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61	38	61.3	58	16	US-10-437-963-193685	Sequence 218138,
62	38	61.3	61	15	US-10-424-599-218138	Sequence 187385,
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66	38	61.3	92	16	US-10-437-963-131043	Sequence 166010,
67	38	61.3	95	15	US-10-424-599-247546	Sequence 153542,
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69	38	61.3	103	15	US-10-424-599-153542	Sequence 166273,
70	38	61.3	103	15	US-10-424-599-179909	Sequence 178342,
71	38	61.3	105	15	US-10-424-599-166273	Sequence 207652,
72	38	61.3	109	15	US-10-424-599-178342	Sequence 234289,
73	38	61.3	109	15	US-10-424-599-234289	Sequence 187427,
74	38	61.3	110	15	US-10-424-599-187427	Sequence 192883,
75	38	61.3	111	15	US-10-424-599-192883	Sequence 187806,
76	38	61.3	116	15	US-10-424-599-187806	Sequence 115875,
77	38	61.3	116	16	US-10-437-963-115875	Sequence 179817,
78	38	61.3	125	16	US-10-437-963-170817	Sequence 207652,
79	38	61.3	126	15	US-10-424-599-207652	Sequence 234289,
80	38	61.3	126	15	US-10-424-599-234289	Sequence 162355,
81	38	61.3	139	15	US-10-424-599-162355	Sequence 117511,
82	38	61.3	139	16	US-10-437-963-117511	Sequence 42048, A
83	38	61.3	139	16	US-10-767-701-42048	Sequence 221095,
84	38	61.3	156	15	US-10-424-599-221095	Sequence 177986,
85	38	61.3	172	15	US-10-424-599-177986	Sequence 246489,
86	38	61.3	217	15	US-10-424-599-246489	

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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:25:00 ; Search time 16.8617 Seconds
(Without alignments)
44.271 Million cell updates/sec

File: us-09-124-280A-19

Perfect score: 62

Sequence: 1 CKKKKFFPFC 10

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

GenClib: 513545 seqs, 74649064 residues

300: 1 number of hits satisfying chosen parameters: 513545

Min DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	42	67.7	140	4	US-09-270-767-33984
5	42	67.7	140	4	US-09-270-767-33984
6	41	66.1	352	4	US-08-979-847B-118
7	41	66.1	378	4	US-08-979-847B-118
8	41	66.1	398	4	US-08-979-847B-121
9	39	62.9	18	3	US-09-100-414B-29
10	39	62.9	18	3	US-09-303-323-29
11	39	62.9	18	3	US-09-770-014-29
12	39	62.9	18	4	US-09-701-588C-29
13	39	62.9	18	4	US-09-747-802-65
14	39	62.9	30	3	US-09-100-414B-69
15	39	62.9	30	3	US-09-303-323-69
16	39	62.9	30	4	US-09-770-014-69
17	39	62.9	30	4	US-09-701-588C-69
18	39	62.9	268	4	US-09-270-767-41047
19	39	62.9	268	4	US-09-270-767-56263
20	38	61.3	29	4	US-09-725-945-3
21	38	61.3	84	4	US-09-270-767-60733
22	38	61.3	148	4	US-09-270-767-60733
23	38	61.3	156	4	US-09-270-767-45241
24	38	61.3	178	4	US-09-270-767-45241
25	38	61.3	204	4	US-09-248-796A-15676
26	38	61.3	329	4	US-09-270-767-44698
27	38	61.3	394	4	US-09-270-767-41074

28	38	61.3	394	4	US-09-270-767-56290	Sequence 56290, A
29	38	61.3	418	4	US-09-725-945-1	Sequence 1, App1
30	38	61.3	638	4	US-09-270-767-46019	Sequence 46019, A
31	37	59.7	65	4	US-09-248-796A-45269	Sequence 25269, A
32	37	59.7	78	4	US-09-248-796A-27340	Sequence 27340, A
33	37	59.7	85	4	US-09-134-000C-3459	Sequence 3459, Ap
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38	36	58.1	30	4	US-09-402-181B-140	Sequence 140, App
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44	36	58.1	137	4	US-09-270-767-51369	Sequence 51369, A
45	36	58.1	151	4	US-09-543-681A-5160	Sequence 5160, Ap
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53	36	58.1	368	4	US-09-438-185A-595	Sequence 595, App
54	36	58.1	399	4	US-09-248-796A-19835	Sequence 19835, A
55	36	58.1	552	3	US-08-851-843A-4	Sequence 4, App1
56	36	58.1	552	3	US-08-854-050-4	Sequence 4, App1
57	36	58.1	552	3	US-09-430-323-4	Sequence 4, App1
58	36	58.1	552	4	US-09-766-253-4	Sequence 4, App1
59	36	58.1	826	4	US-09-949-016-9212	Sequence 9212, Ap
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61	36	58.1	826	4	US-09-949-016-9214	Sequence 9214, Ap
62	35	56.5	10	3	US-08-477-778-14	Sequence 14, App
63	35	56.5	62	4	US-09-270-767-46686	Sequence 46686, A
64	35	56.5	62	4	US-09-270-767-62297	Sequence 62297, A
65	35	56.5	66	4	US-09-248-796A-26828	Sequence 26828, A
66	35	56.5	67	4	US-09-270-767-44621	Sequence 44621, A
67	35	56.5	92	4	US-09-248-796A-25181	Sequence 25181, A
68	35	56.5	100	4	US-09-248-796A-21060	Sequence 21060, A
69	35	56.5	143	4	US-09-270-767-44294	Sequence 44294, A
70	35	56.5	160	4	US-09-270-767-42225	Sequence 42225, A
71	35	56.5	162	4	US-09-270-767-57842	Sequence 57842, A
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73	35	56.5	268	4	US-09-270-767-58322	Sequence 58322, A
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76	35	56.5	558	4	US-09-107-532A-7161	Sequence 43341, A
77	35	56.5	597	4	US-09-252-991A-31342	Sequence 31342, A
78	35	56.5	1244	4	US-10-164-596-24	Sequence 24, App1
79	34	54.8	16	4	US-09-541-345-94	Sequence 94, App1
80	34	54.8	27	4	US-09-428-082B-582	Sequence 582, App
81	34	54.8	44	4	US-09-270-767-34152	Sequence 34152, A
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86	34	54.8	84	4	US-09-621-976-5846	Sequence 5846, Ap
87	34	54.8	100	4	US-09-248-796A-22482	Sequence 22482, A
88	34	54.8	110	4	US-09-248-796A-22496	Sequence 22496, A
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93	34	54.8	235	4	US-09-248-796A-19719	Sequence 19719, A
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OM protein - protein search, using SW model

Run on: March 26, 2005, 10:43:56 ; Search time 43.0851 Seconds
(without alignments)
76.848 Million cell updates/sec

US-09-124-280a-18

Perfect score: 60

Sequence: 1 KCKKKKKCK 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1407402 seqs, 33110923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	40	66.7	179	16	US-10-437-963-188183
6	40	66.7	185	16	US-10-437-963-115253
7	40	66.7	289	15	US-10-149-310-212
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9	38	63.3	70	15	US-10-424-599-203514
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11	38	63.3	409	9	US-09-908-711-122
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16	38	63.3	446	10	US-09-796-753-88	Sequence 88, App
17	38	63.3	446	14	US-10-247-451-1	Sequence 1, App
18	38	63.3	446	15	US-10-247-451-1	Sequence 1, App
19	38	63.3	446	15	US-10-247-451-1	Sequence 1, App
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22	38	63.3	830	17	US-10-741-849-7088	Sequence 7088, App
23	38	63.3	1146	9	US-09-994-485-6	Sequence 6, App
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25	37	61.7	45	15	US-10-424-599-255019	Sequence 255019, App
26	37	61.7	65	14	US-10-106-698-5432	Sequence 5432, App
27	37	61.7	829	15	US-09-801-368-324	Sequence 324, App
28	37	61.7	829	15	US-10-149-310-204	Sequence 204, App
29	37	61.7	904	15	US-09-801-368-272	Sequence 272, App
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32	36	60.0	62	16	US-10-767-701-47669	Sequence 47669, App
33	36	60.0	65	16	US-10-767-701-55544	Sequence 55544, App
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35	36	60.0	151	9	US-09-764-868-673	Sequence 673, App
36	36	60.0	151	9	US-09-764-868-1096	Sequence 1096, App
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39	36	60.0	235	14	US-09-794-257-2	Sequence 2, App
40	36	60.0	236	15	US-10-330-372-3	Sequence 3, App
41	36	60.0	236	15	US-10-400-991-61	Sequence 61, App
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44	36	60.0	239	15	US-10-295-027-220	Sequence 220, App
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46	36	60.0	390	15	US-10-425-114-46204	Sequence 46204, App
47	36	60.0	517	15	US-10-425-114-48947	Sequence 48947, App
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63	35	58.3	147	9	US-09-965-703-44	Sequence 44, App
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83	35	58.3	268	15	US-10-149-310-782	Sequence 282, App
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85	35	58.3	283	15	US-10-276-289-7	Sequence 7, App
86	35	58.3	308	17	US-10-849-423-14	Sequence 14, App

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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:25:00 ; Search time 16.8617 Seconds
(without alignments)
44.271 Million cell updates/sec

Target: US-09-124-280a-18

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Search table: BLOSUM62

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Number of hits satisfying chosen parameters: 513545

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Postprocessing: Minimum Match 0%

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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	38	63.3	188 4 US-09-248-796A-1895	Sequence 1895, A
6	38	63.3	205 4 US-09-248-796A-18923	Sequence 18923, A
7	38	63.3	232 4 US-09-248-796A-18894	Sequence 18894, A
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9	38	63.3	1146 3 US-08-914-999-6	Sequence 6, Appl
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11	37	61.7	439 4 US-09-248-796A-18964	Sequence 18964, A
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16	35	58.3	54 4 US-09-270-767-37907	Sequence 37907, A
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OM protein - protein search, using SW model

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(without alignments)
76.848 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	43	72.9	453	US-10-437-963-20216	Sequence 202716,
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4	40	67.8	99	US-10-437-963-127665	Sequence 127665,
5	40	67.8	282	US-10-437-963-108435	Sequence 108435,
6	39	66.1	95	US-10-767-701-47798	Sequence 47798, A
7	39	66.1	105	US-10-437-963-185808	Sequence 185808,
8	39	66.1	111	US-10-437-963-119890	Sequence 119890,
9	39	66.1	125	US-10-437-963-142630	Sequence 142630,
10	39	66.1	146	US-10-437-963-107023	Sequence 107023,
11	39	66.1	2068	US-10-437-963-106878	Sequence 106878,
12	39	66.1	19608	US-10-084-846A-8	Sequence 8, Appl1
13	38	64.4	41	US-09-864-761-33583	Sequence 33583, A

14	38	64.4	50	US-10-437-963-158814	Sequence 158814,
15	38	64.4	191	US-10-424-589-247454	Sequence 247454,
16	38	64.4	202	US-10-437-963-108985	Sequence 108985,
17	38	64.4	216	US-10-425-114-71383	Sequence 71383, A
18	38	64.4	278	US-10-425-114-61229	Sequence 61229, A
19	37	62.7	10	US-09-124-280A-31	Sequence 31, Appl
20	37	62.7	11	US-09-124-280A-35	Sequence 35, Appl
21	37	62.7	13	US-10-451-795-10	Sequence 10, Appl
22	37	62.7	14	US-10-451-795-8	Sequence 9, Appl1
23	37	62.7	17	US-10-437-963-105539	Sequence 105539,
24	37	62.7	82	US-10-437-963-163542	Sequence 163542,
25	37	62.7	98	US-10-437-963-163542	Sequence 163542,
26	37	62.7	106	US-10-437-963-195253	Sequence 508, App
27	37	62.7	115	US-09-939-980-508	Sequence 52201, A
28	37	62.7	134	US-10-425-114-52201	Sequence 165552,
29	37	62.7	149	US-10-437-963-165552	Sequence 198768,
30	37	62.7	212	US-10-437-963-198768	Sequence 163328,
31	37	62.7	380	US-10-437-963-163328	Sequence 55954, A
32	37	62.7	447	US-10-425-114-55954	Sequence 192, App
33	37	62.7	465	US-10-114-270-192	Sequence 14702, A
34	37	62.7	568	US-10-369-493-14402	Sequence 14771, A
35	37	62.7	568	US-10-369-493-14771	Sequence 189011,
36	37	62.7	669	US-10-424-599-189011	Sequence 121124,
37	37	62.7	741	US-10-437-963-118054	Sequence 121124,
38	37	62.7	821	US-10-437-963-121124	Sequence 228645,
39	36	61.0	58	US-10-424-599-228645	Sequence 201299,
40	36	61.0	78	US-10-437-963-201299	Sequence 197522,
41	36	61.0	79	US-10-424-599-197522	Sequence 170358,
42	36	61.0	79	US-10-437-963-170358	Sequence 120789,
43	36	61.0	89	US-10-437-963-120789	Sequence 3360, Ap
44	36	61.0	110	US-09-864-408A-3360	Sequence 33926, A
45	36	61.0	126	US-10-767-701-33926	Sequence 112055,
46	36	61.0	169	US-10-437-963-112055	Sequence 112055,
47	36	61.0	189	US-10-437-963-112056	Sequence 206, App
48	36	61.0	210	US-09-764-846-206	Sequence 60150, A
49	36	61.0	232	US-10-091-483-206	Sequence 76052, A
50	36	61.0	304	US-10-425-114-60150	Sequence 2, Appl1
51	36	61.0	381	US-10-184-832-2	Sequence 55121, A
52	36	61.0	383	US-10-184-832-2	Sequence 16, Appl
53	36	61.0	424	US-10-425-114-55121	Sequence 17, Appl
54	36	61.0	424	US-10-770-600-17	Sequence 18, Appl
55	36	61.0	424	US-10-770-600-18	Sequence 139435,
56	36	61.0	470	US-10-437-963-139435	Sequence 2470, Ap
57	36	61.0	479	US-10-408-766A-2470	Sequence 388, App
58	36	61.0	511	US-10-221-625-99	Sequence 99, Appl
59	36	61.0	536	US-10-363-616-388	Sequence 143634,
60	36	61.0	536	US-10-424-599-143634	Sequence 131, App
61	36	61.0	826	US-10-126-103-131	Sequence 131, App
62	36	61.0	826	US-10-431-096-131	Sequence 54012, A
63	36	61.0	866	US-10-282-122A-54012	Sequence 2, Appl1
64	36	61.0	872	US-10-332-284A-2	Sequence 6, Appl1
65	36	61.0	1116	US-10-332-284A-2	Sequence 4, Appl1
66	36	61.0	1116	US-10-332-284A-4	Sequence 8, Appl1
67	36	61.0	1616	US-10-332-284A-4	Sequence 8, Appl1
68	36	61.0	1616	US-10-332-284A-8	Sequence 107633,
69	36	61.0	2050	US-10-437-963-107633	Sequence 315, App
70	35.5	60.2	47	US-10-178-213-315	Sequence 327, App
71	35.5	60.2	47	US-10-178-213-327	Sequence 337, App
72	35.5	60.2	47	US-10-178-213-333	Sequence 362, App
73	35.5	60.2	47	US-10-178-213-362	Sequence 362, App
74	35.5	60.2	47	US-10-178-213-363	Sequence 399, App
75	35.5	60.2	47	US-10-178-213-399	Sequence 402, App
76	35.5	60.2	47	US-10-178-213-402	Sequence 429, App
77	35.5	60.2	47	US-10-178-213-429	Sequence 405, App
78	35.5	60.2	48	US-10-178-213-405	Sequence 401, App
79	35.5	60.2	75	US-10-178-213-401	Sequence 404, App
80	35.5	60.2	76	US-10-178-213-404	Sequence 428, App
81	35.5	60.2	76	US-10-178-213-428	Sequence 398, App
82	35.5	60.2	77	US-10-178-213-398	Sequence 314, App
83	35.5	60.2	78	US-10-178-213-314	Sequence 326, App
84	35.5	60.2	79	US-10-178-213-326	Sequence 332, App
85	35.5	60.2	79	US-10-178-213-332	Sequence 178547,
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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:25:00 ; Search time 16.8617 Seconds
(without alignments)
44.271 Million cell updates/sec

Title: US-09-124-280A-17

Perfect score: 59

Sequence: 1 RTTCRFRRRC 10

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Sequences: 513545 seqs, 74649064 residues

Number of hits satisfying chosen parameters: 513545

Min DB seq length: 0

Max DB seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	59	100.0	10	1	US-08-097-830E-17
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5	39	66.1	342	4	US-09-252-991A-32031
6	38	64.4	160	4	US-09-270-767-45604
7	38	64.4	209	4	US-09-252-991A-21363
8	38	64.4	446	4	US-09-252-991A-31114
9	37.5	63.6	236	4	US-09-248-796A-19564
10	37	62.7	10	1	US-08-049-871-2
11	37	62.7	10	1	US-07-819-893-2
12	37	62.7	10	1	US-08-280-397-2
13	37	62.7	10	1	US-08-218-026-49
14	37	62.7	10	2	US-08-653-632-49
15	37	62.7	10	2	US-08-456-112B-31
16	37	62.7	11	1	US-08-049-871-6
17	37	62.7	11	1	US-07-819-893-6
18	37	62.7	11	1	US-08-280-397-6
19	37	62.7	11	1	US-08-218-026-50
20	37	62.7	11	2	US-08-653-632-50
21	37	62.7	11	2	US-08-456-112B-35
22	37	62.7	83	4	US-09-489-039A-10524
23	37	62.7	115	4	US-08-936-165A-508
24	37	62.7	142	4	US-09-489-039A-9237
25	37	62.7	863	4	US-09-252-991A-21831
26	36	61.0	109	4	US-09-270-767-41290
27	36	61.0	109	4	US-09-270-767-56506

28	36	61.0	124	4	US-09-270-767-48315	Sequence 48315, A
29	36	61.0	161	4	US-09-252-991A-17199	Sequence 17199, A
30	36	61.0	172	4	US-09-252-991A-23710	Sequence 23710, A
31	36	61.0	193	4	US-09-270-767-33468	Sequence 33468, A
32	36	61.0	215	4	US-09-252-991A-19924	Sequence 19924, A
33	36	61.0	362	4	US-09-252-991A-31349	Sequence 31349, A
34	36	61.0	406	4	US-09-252-991A-24973	Sequence 24973, A
35	36	61.0	418	4	US-09-252-991A-29452	Sequence 29452, A
36	36	61.0	470	4	US-09-270-767-61004	Sequence 61004, A
37	36	61.0	601	4	US-09-270-767-45496	Sequence 45496, A
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41	35	59.3	32	4	US-09-030-619-193	Sequence 193, Appl
42	35	59.3	32	4	US-09-917-340-48	Sequence 48, Appl
43	35	59.3	100	4	US-09-732-210-1168	Sequence 1168, Appl
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51	35	59.3	451	4	US-09-252-991A-29903	Sequence 29903, A
52	35	59.3	455	3	US-09-038-217A-18	Sequence 18, Appl
53	35	59.3	455	3	US-09-447-034-18	Sequence 18, Appl
54	35	59.3	465	3	US-08-927-219-79	Sequence 79, Appl
55	35	59.3	471	4	US-09-949-016-10293	Sequence 10293, A
56	35	59.3	516	3	US-08-927-219-140	Sequence 140, Appl
57	35	59.3	567	3	US-09-270-767-39674	Sequence 39674, A
58	34	57.6	73	4	US-09-270-767-54891	Sequence 54891, A
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61	34	57.6	142	4	US-09-252-991A-26738	Sequence 26738, A
62	34	57.6	151	4	US-09-270-767-37857	Sequence 37857, A
63	34	57.6	151	4	US-09-270-767-53074	Sequence 53074, A
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65	34	57.6	165	4	US-09-252-991A-20304	Sequence 20304, A
66	34	57.6	168	4	US-09-252-991A-29614	Sequence 29614, A
67	34	57.6	196	4	US-09-252-991A-26368	Sequence 26368, A
68	34	57.6	208	4	US-09-252-991A-29277	Sequence 29277, A
69	34	57.6	218	4	US-09-849-016-8395	Sequence 8395, Appl
70	34	57.6	271	4	US-09-252-991A-26235	Sequence 26235, Appl
71	34	57.6	301	2	US-08-656-906-25	Sequence 25, Appl
72	34	57.6	301	3	US-09-217-847-25	Sequence 25, Appl
73	34	57.6	322	4	US-09-252-991A-31782	Sequence 31782, A
74	34	57.6	469	4	US-09-252-991A-32910	Sequence 32910, A
75	34	57.6	469	3	US-09-336-643A-8	Sequence 8, Appl
76	34	57.6	551	4	US-09-252-991A-22694	Sequence 22694, A
77	34	57.6	639	4	US-09-252-991A-28570	Sequence 28570, A
78	34	57.6	714	4	US-09-252-991A-28806	Sequence 28806, A
79	34	57.6	793	4	US-09-270-767-36730	Sequence 36730, A
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81	34	57.6	793	4	US-09-538-092-10077	Sequence 10077, Appl
82	34	57.6	966	4	US-09-252-991A-19087	Sequence 19087, A
83	33.5	56.8	348	4	US-08-472-219-1	Sequence 1, Appl
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86	33	55.9	106	4	US-08-469-260A-253	Sequence 253, Appl
87	33	55.9	106	4	US-08-488-446-253	Sequence 253, Appl
88	33	55.9	106	4	US-08-467-344A-253	Sequence 253, Appl
89	33	55.9	106	4	US-08-424-508B-253	Sequence 253, Appl
90	33	55.9	106	4	US-10-101-464A-828	Sequence 828, Appl
91	33	55.9	129	4	US-09-252-991A-16959	Sequence 16959, A
92	33	55.9	134	4	US-09-252-991A-22336	Sequence 22336, A
93	33	55.9	135	4	US-09-339-614-2	Sequence 2, Appl
94	33	55.9	146	4	US-09-252-991A-16646	Sequence 16646, A
95	33	55.9	154	4	US-09-252-991A-17526	Sequence 17526, A
96	33	55.9	167	4	US-09-949-016-10231	Sequence 10231, A
97	33	55.9	202	4	US-09-270-767-45622	Sequence 45622, A
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OM protein - protein search, using SW model

Run on: March 26, 2005, 10:43:56 ; Search time 43.0851 seconds

(without alignments)
76.848 Million cell updates/sec

Title: US-09-124-280A-16

Perfect score: 55

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Number of hits satisfying chosen parameters: 1407402

Min. DB seq length: 0

Max. NumDB seq length: 200000000

Seq. processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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7	38	69.1	538 15 US-10-282-122A-63743	Sequence 63743, A
8	38	69.1	975 16 US-10-437-963-186445	Sequence 186445,
9	37	67.3	76 15 US-10-424-599-254879	Sequence 254879,
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11	36	65.5	93 15 US-10-424-599-249862	Sequence 249862,
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22	35	63.6	233 15 US-10-282-122A-77803	Sequence 77803, A
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27	35	63.6	547 14 US-10-245-107-40	Sequence 40, Appl
28	35	63.6	547 14 US-10-245-143-40	Sequence 40, Appl
29	35	63.6	547 14 US-10-245-771-40	Sequence 40, Appl
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OM protein - protein search, using SW model

Run on: March 26, 2005, 10:25:00 ; Search time 16.8617 Seconds
(without alignments)
44.271 Million cell updates/sec

Title: US-09-124-280A-16
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Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

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Total number of hits satisfying chosen parameters: 513545

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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
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US-09-124-280A-15

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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US-09-124-280a-15
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Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: /cgn2_6/ptcdatara/1/aa/5A_COMB.pep.*
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6: /cgn2_6/ptcdatara/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	10	1	US-08-097-830E-15
2	61	100.0	10	2	US-08-456-112B-15
3	43	70.5	10	1	US-08-097-830E-16
4	43	70.5	10	2	US-08-456-112B-16
5	41	67.2	10	1	US-08-097-830E-5
6	41	67.2	10	2	US-08-456-112B-5
7	39.5	64.8	10	1	US-08-097-830E-18
8	39.5	64.8	10	2	US-08-456-112B-18
9	39	63.9	33	4	US-09-270-767-56458
10	39	63.9	33	3	US-09-270-767-56458
11	39	63.9	35	3	US-09-518-046-13
12	39	63.9	294	3	US-09-518-046-4
13	39	63.9	454	3	US-09-518-046-2
14	39	63.9	455	3	US-09-261-416-2
15	39	63.9	521	4	US-09-949-016-11081
16	39	63.9	521	4	US-09-949-016-11082
17	39	63.9	521	4	US-09-949-016-11083
18	37	60.7	10	1	US-08-049-871-2
19	37	60.7	10	1	US-07-819-893-2
20	37	60.7	10	1	US-08-280-397-2
21	37	60.7	10	1	US-08-218-026-49
22	37	60.7	10	2	US-08-653-632-49
23	37	60.7	10	2	US-08-456-112B-31
24	37	60.7	11	1	US-08-049-871-6
25	37	60.7	11	1	US-07-819-893-6
26	37	60.7	11	1	US-08-280-397-6
27	37	60.7	11	1	US-08-218-026-50

28	37	60.7	11	2	US-08-653-632-50	Sequence 50, App1
29	37	60.7	11	2	US-08-456-112B-13	Sequence 13, App1
30	37	60.7	11	2	US-08-456-112B-35	Sequence 35, App1
31	37	60.7	128	4	US-09-248-796A-27972	Sequence 27972, A
32	37	60.7	253	4	US-09-270-767-48906	Sequence 48906, A
33	36	59.0	10	2	US-08-456-112B-43	Sequence 43, App1
34	36	59.0	123	4	US-09-270-767-38027	Sequence 38027, A
35	36	59.0	123	4	US-09-270-767-53244	Sequence 53244, A
36	36	59.0	226	4	US-09-270-767-37148	Sequence 37148, A
37	36	59.0	226	4	US-09-270-767-53365	Sequence 53365, A
38	36	59.0	253	4	US-09-270-767-33689	Sequence 33689, A
39	35.5	58.2	62	4	US-09-107-532A-5924	Sequence 5924, Ap
40	35	57.4	91	4	US-09-248-796A-22642	Sequence 22642, A
41	35	57.4	150	4	US-09-328-352-6423	Sequence 6423, Ap
42	35	57.4	652	2	US-08-751-305-2	Sequence 2, App1
43	34	55.7	9	3	US-09-518-046-126	Sequence 126, App
44	34	55.7	20	4	US-09-615-153-5	Sequence 5, App1
45	34	55.7	55	4	US-09-270-767-58360	Sequence 58360, A
46	34	55.7	58	4	US-10-108-311-8	Sequence 8, App1
47	34	55.7	60	4	US-09-270-767-60389	Sequence 60389, A
48	34	55.7	66	4	US-09-248-796A-22637	Sequence 22637, A
49	34	55.7	76	4	US-09-270-767-33955	Sequence 33955, A
50	34	55.7	76	4	US-09-270-767-49172	Sequence 49172, A
51	34	55.7	149	4	US-09-270-767-43030	Sequence 43030, A
52	34	55.7	263	1	US-07-906-983-2	Sequence 2, App1
53	34	55.7	263	1	US-09-653-813-2	Sequence 2, App1
54	34	55.7	288	4	US-09-270-767-44915	Sequence 44915, A
55	34	55.7	341	4	US-09-248-796A-14575	Sequence 14575, A
56	34	55.7	686	4	US-09-248-796A-17659	Sequence 17659, A
57	33	54.1	53	4	US-09-270-767-61282	Sequence 61282, A
58	33	54.1	73	4	US-09-248-796A-21776	Sequence 21776, A
59	33	54.1	83	4	US-09-489-039A-10524	Sequence 10524, A
60	33	54.1	107	4	US-09-270-767-31707	Sequence 31707, A
61	33	54.1	107	4	US-09-270-767-46924	Sequence 46924, A
62	33	54.1	145	4	US-09-270-767-53356	Sequence 53356, A
63	33	54.1	145	4	US-09-270-767-50573	Sequence 50573, A
64	33	54.1	150	4	US-09-270-767-46076	Sequence 46076, A
65	33	54.1	200	4	US-09-134-000C-3505	Sequence 3505, Ap
66	33	54.1	211	4	US-09-513-999C-5216	Sequence 5216, Ap
67	33	54.1	226	3	US-09-299-378-2	Sequence 2, App1
68	33	54.1	275	4	US-09-248-796A-20688	Sequence 20688, A
69	33	54.1	326	4	US-09-328-352-5570	Sequence 5570, Ap
70	33	54.1	330	4	US-09-328-352-6175	Sequence 6175, Ap
71	33	54.1	348	4	US-09-248-796A-20983	Sequence 20983, A
72	33	54.1	355	4	US-09-270-767-37109	Sequence 37109, A
73	33	54.1	355	4	US-09-270-767-53326	Sequence 53326, A
74	33	54.1	4654	3	US-08-476-515A-84	Sequence 84, App1
75	33	54.1	4655	3	US-08-652-877-84	Sequence 84, App1
76	33	54.1	4655	3	US-08-652-877-86	Sequence 86, App1
77	33	54.1	4655	3	US-08-652-877-88	Sequence 88, App1
78	33	54.1	4655	3	US-08-652-877-90	Sequence 90, App1
79	32	52.5	10	1	US-08-097-830E-17	Sequence 17, App1
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81	32	52.5	27	4	US-09-489-847-307	Sequence 307, App
82	32	52.5	37	4	US-09-894-882-60	Sequence 60, App1
83	32	52.5	37	4	US-09-894-882-427	Sequence 427, App
84	32	52.5	55	4	US-09-621-976-6004	Sequence 6004, App
85	32	52.5	68	4	US-09-497-822C-15	Sequence 15, App1
86	32	52.5	72	4	US-09-248-796A-25443	Sequence 25443, A
87	32	52.5	83	4	US-09-107-532A-1777	Sequence 1777, Ap
88	32	52.5	84	4	US-09-540-236-2784	Sequence 2784, Ap
89	32	52.5	88	4	US-09-270-767-35764	Sequence 35764, A
90	32	52.5	88	4	US-09-270-767-55981	Sequence 55981, A
91	32	52.5	88	4	US-09-248-796A-27021	Sequence 27021, A
92	32	52.5	103	4	US-09-248-796A-24161	Sequence 24161, A
93	32	52.5	124	4	US-09-270-767-48315	Sequence 48315, A
94	32	52.5	125	4	US-09-270-767-33098	Sequence 33098, A
95	32	52.5	133	4	US-09-270-767-37757	Sequence 37757, A
96	32	52.5	133	4	US-09-270-767-52974	Sequence 52974, A
97	32	52.5	155	4	US-09-270-767-58814	Sequence 58814, A
98	32	52.5	158	4	US-09-270-767-36149	Sequence 36149, A
99	32	52.5	158	4	US-09-270-767-51366	Sequence 51366, A
100	32	52.5	166	4	US-09-489-847-148	Sequence 148, App

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 26, 2005, 10:43:56 ; Search time 25.8511 Seconds
(Without alignments)
76.848 Million cell updates/sec

Title: US-09-124-280A-14

Perfect score: 39

Sequence: 1 CKEFKC 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Beam check: 1407402 seqs, 311100923 residues

Min. num DB seq length: 0

Max. num DB seq length: 2000000000

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database: Published Applications AA.*

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6: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pep.*
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20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	100.0	6	9	US-09-124-280A-14
2	36	92.3	83	10	US-09-814-604-20
3	36	92.3	83	10	US-09-922-226-6
4	36	92.3	83	10	US-09-922-226-159
5	36	92.3	103	13	US-10-317-832-121
6	36	92.3	198	13	US-10-087-192-588
7	36	92.3	219	9	US-09-925-201-957
8	36	92.3	322	9	US-09-965-529-9
9	36	92.3	322	10	US-09-969-680A-9
10	36	92.3	322	14	US-10-197-666A-16
11	36	92.3	322	14	US-10-024-298A-37
12	36	92.3	322	14	US-10-042-211A-37
13	36	92.3	322	15	US-10-617-217A-37

14	36	92.3	342	13	US-10-087-192-585	Sequence 585, App
15	36	92.3	360	15	US-10-264-049-2959	Sequence 2959, App
16	36	92.3	451	15	US-10-287-226-376	Sequence 376, App
17	36	92.3	458	15	US-10-287-226-378	Sequence 378, App
18	36	92.3	490	15	US-10-435-696-41	Sequence 41, App1
19	36	92.3	490	15	US-10-425-114-72781	Sequence 72781, A
20	36	92.3	490	15	US-10-425-114-72798	Sequence 72798, A
21	36	92.3	560	15	US-10-616-897-11	Sequence 11, App1
22	36	92.3	614	15	US-10-435-696-42	Sequence 42, App1
23	36	92.3	621	17	US-10-501-525-4	Sequence 4, App1
24	36	92.3	621	15	US-10-425-114-72946	Sequence 72946, A
25	36	92.3	621	15	US-10-425-114-72947	Sequence 72947, A
26	36	92.3	76	15	US-10-424-559-281036	Sequence 281036, A
27	36	89.7	715	14	US-10-028-072-116	Sequence 116, App
28	36	89.7	715	14	US-10-140-808-116	Sequence 116, App
29	36	89.7	715	14	US-10-121-049-116	Sequence 116, App
30	36	89.7	715	14	US-10-123-904-116	Sequence 116, App
31	36	89.7	715	14	US-10-140-474-116	Sequence 116, App
32	36	89.7	715	14	US-10-142-431-116	Sequence 116, App
33	36	89.7	715	14	US-10-175-746-116	Sequence 116, App
34	36	89.7	715	14	US-10-176-918-116	Sequence 116, App
35	36	89.7	715	14	US-10-176-921-116	Sequence 116, App
36	36	89.7	715	14	US-10-137-865-116	Sequence 116, App
37	36	89.7	715	14	US-10-140-474-116	Sequence 116, App
38	36	89.7	715	14	US-10-143-114-116	Sequence 116, App
39	36	89.7	715	14	US-10-142-419-116	Sequence 116, App
40	36	89.7	715	14	US-10-123-262-116	Sequence 116, App
41	36	89.7	715	14	US-10-142-423-116	Sequence 116, App
42	36	89.7	715	14	US-10-121-050-116	Sequence 116, App
43	36	89.7	715	14	US-10-141-755-116	Sequence 116, App
44	36	89.7	715	14	US-10-143-032-116	Sequence 116, App
45	36	89.7	715	14	US-10-123-108-116	Sequence 116, App
46	36	89.7	715	14	US-10-123-226-116	Sequence 116, App
47	36	89.7	715	14	US-10-123-226-116	Sequence 116, App
48	36	89.7	715	14	US-10-140-921-116	Sequence 116, App
49	36	89.7	715	14	US-10-140-928-116	Sequence 116, App
50	36	89.7	715	14	US-10-121-045-116	Sequence 116, App
51	36	89.7	715	14	US-10-123-232-116	Sequence 116, App
52	36	89.7	715	14	US-10-123-903-116	Sequence 116, App
53	36	89.7	715	14	US-10-124-819-116	Sequence 116, App
54	36	89.7	715	14	US-10-124-822-116	Sequence 116, App
55	36	89.7	715	14	US-10-140-925-116	Sequence 116, App
56	36	89.7	715	14	US-10-160-498-116	Sequence 116, App
57	36	89.7	715	14	US-10-124-824-116	Sequence 116, App
58	36	89.7	715	14	US-10-127-825A-116	Sequence 116, App
59	36	89.7	715	14	US-10-127-829A-116	Sequence 116, App
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63	36	89.7	715	14	US-10-127-845A-116	Sequence 116, App
64	36	89.7	715	14	US-10-128-693A-116	Sequence 116, App
65	36	89.7	715	14	US-10-131-813A-116	Sequence 116, App
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81	36	89.7	715	14	US-10-147-531-116	Sequence 116, App
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83	36	89.7	715	14	US-10-147-533-116	Sequence 116, App
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85	36	89.7	715	14	US-10-147-535-116	Sequence 116, App
86	36	89.7	715	14	US-10-147-536-116	Sequence 116, App

Gencore version 5.1.6
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OM Protein - protein search, using sw model

March 26, 2005, 10:25:00 ; Search time 10.117 Seconds

(without alignments)
44.271 Million cell updates/sec

Run on: US-09-124-280A-14

Ref. seq. score: 39

Seq. id: 1 CKEKCC 6

Seq. gap table: BLOSUM62

Gapop 10.0, Gapext 0.5

Seq. id: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	39	100.0	6	1	US-08-097-830E-14
2	39	100.0	6	2	US-08-456-112B-14
3	36	92.3	68	4	US-09-497-822C-15
4	36	92.3	68	4	US-09-497-822C-16
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6	36	92.3	355	6	5223606-4
7	36	92.3	410	3	US-08-764-870-1
8	36	92.3	410	3	US-08-764-870-2
9	36	92.3	410	3	US-08-980-115-1
10	36	92.3	410	3	US-08-980-115-2
11	36	92.3	410	6	5438126-2
12	36	92.3	410	6	5438126-2
13	36	92.3	461	3	US-08-764-870-3
14	36	92.3	461	3	US-08-980-115-3
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17	36	92.3	560	3	US-09-510-654-10
18	36	92.3	621	4	US-09-949-016-11557
19	36	92.3	6	1	US-08-097-830E-32
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32	32	82.1	225	4	US-09-425-021-22	Sequence 22, Appl
33	32	82.1	225	4	US-09-229-947-25	Sequence 25, Appl
34	32	82.1	225	4	US-09-564-829-16	Sequence 16, Appl
35	32	82.1	225	4	US-09-490-714-13	Sequence 3, Appl
36	32	82.1	225	4	US-09-490-714-10	Sequence 10, Appl
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49	32	82.1	441	3	US-08-764-870-9	Sequence 9, Appl
50	32	82.1	441	3	US-08-980-115-9	Sequence 9, Appl
51	32	82.1	441	3	US-09-976-594-1000	Sequence 1000, Ap
52	32	82.1	441	4	US-09-166-265-7	Sequence 7, Appl
53	32	82.1	466	4	US-09-949-016-9704	Sequence 9704, Ap
54	32	82.1	475	2	US-08-484-200-2	Sequence 2, Appl
55	32	82.1	475	2	US-08-465-375-2	Sequence 2, Appl
56	32	82.1	475	3	US-08-764-870-10	Sequence 10, Appl
57	32	82.1	475	3	US-08-980-115-10	Sequence 10, Appl
58	32	82.1	475	4	US-09-788-070-2	Sequence 2, Appl
59	32	82.1	475	4	US-10-142-373-2	Sequence 2, Appl
60	32	82.1	475	4	US-09-587-549C-2	Sequence 2, Appl
61	32	82.1	475	4	US-09-155-252A-2	Sequence 2, Appl
62	32	82.1	476	3	US-08-134-557D-2	Sequence 2, Appl
63	32	82.1	477	3	US-09-128-142-2	Sequence 2, Appl
64	32	82.1	478	4	US-09-166-265-5	Sequence 5, Appl
65	32	82.1	478	4	US-09-765-111A-27	Sequence 27, Appl
66	32	82.1	495	2	US-09-132-619-2	Sequence 2, Appl
67	32	82.1	495	2	US-09-382-803B-2	Sequence 2, Appl
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69	32	82.1	495	4	US-09-949-016-6419	Sequence 6419, Ap
70	32	82.1	500	2	US-09-132-619-8	Sequence 8, Appl
71	32	82.1	500	3	US-09-282-803B-8	Sequence 8, Appl
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73	32	82.1	500	4	US-09-949-016-11597	Sequence 11597, A
74	32	82.1	505	3	US-09-128-142-4	Sequence 4, Appl
75	32	82.1	505	4	US-09-765-111A-16	Sequence 16, Appl
76	32	82.1	505	4	US-09-949-016-7067	Sequence 7067, Ap
77	32	82.1	506	3	US-09-514-247A-6	Sequence 6, Appl
78	32	82.1	521	4	US-09-949-016-9620	Sequence 9620, Ap
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82	32	82.1	541	3	US-09-510-654-6	Sequence 6, Appl
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84	32	82.1	541	4	US-09-949-016-10338	Sequence 10338, A
85	32	82.1	617	4	US-09-949-016-6776	Sequence 6776, Ap
86	32	82.1	626	4	US-09-949-016-6776	Sequence 10263, A
87	32	82.1	626	4	US-09-949-016-1063	Sequence 9660, Ap
88	32	82.1	697	4	US-09-949-016-9660	Sequence 2, Appl
89	32	82.1	777	4	US-09-765-111A-23	Sequence 23, Appl
90	32	82.1	811	4	US-09-765-111A-4	Sequence 4, Appl
91	32	82.1	811	4	US-09-765-111A-4	Sequence 4, Appl
92	32	82.1	874	4	US-09-165-111A-6	Sequence 6, Appl
93	31	79.5	9	3	US-09-139-802-151	Sequence 151, App
94	31	79.5	9	4	US-08-926-914-151	Sequence 151, App
95	31	79.5	9	4	US-09-659-786-151	Sequence 27880, A
96	31	79.5	67	4	US-09-248-796A-27880	Sequence 33664, A
97	31	79.5	253	4	US-09-270-767-33664	Sequence 19664, A
98	31	79.5	257	4	US-09-248-796A-19664	Sequence 1830, Ap
99	31	79.5	266	3	US-09-134-001C-4830	Sequence 1480, Ap
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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:43:56 Search time 47.3936 Seconds

(without alignments)
76.848 Million cell updates/sec

Title: US-09-124-280A-13

Perfect score: 79

Sequence: 1 CKCKCKCKCKC 11

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	55	69.6	290	16	US-10-437-963-157903
5	54	68.4	423	14	US-10-017-161-2118
6	54	68.4	423	15	US-10-292-798-1764
7	53	67.1	105	16	US-10-437-963-120482
8	51	64.6	285	15	US-10-369-493-4103
9	50	63.3	13	10	US-09-302-517-19
10	50	63.3	13	15	US-10-402-021-19
11	50	63.3	140	14	US-10-062-548-71
12	50	63.3	140	17	US-10-918-446-71
13	49	62.0	11	9	US-09-782-960-128

14	49	62.0	11	16	US-10-806-018-128	Sequence 128, App
15	49	62.0	44	15	US-10-424-559-202469	Sequence 202469, App
16	49	62.0	60	16	US-10-437-963-149100	Sequence 149100, App
17	49	62.0	75	15	US-10-424-559-191997	Sequence 191997, App
18	49	62.0	609	16	US-10-437-963-195733	Sequence 195733, App
19	49	62.0	695	14	US-10-184-644-567	Sequence 567, App
20	49	62.0	695	14	US-10-184-644-567	Sequence 567, App
21	49	62.0	1069	15	US-10-307-817-521	Sequence 521, App
22	49	62.0	1536	14	US-10-184-644-461	Sequence 461, App
23	49	62.0	1536	14	US-10-184-644-461	Sequence 461, App
24	49	62.0	1647	14	US-10-123-155-191	Sequence 191, App
25	49	62.0	1647	14	US-10-146-731-191	Sequence 191, App
26	49	62.0	1647	14	US-10-146-731-191	Sequence 191, App
27	49	62.0	1647	14	US-10-146-731-191	Sequence 191, App
28	49	62.0	1647	14	US-10-146-731-191	Sequence 191, App
29	49	62.0	1647	14	US-10-146-731-191	Sequence 191, App
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32	49	62.0	1647	15	US-10-141-759-191	Sequence 191, App
33	49	62.0	1647	15	US-10-141-759-191	Sequence 191, App
34	49	62.0	1647	15	US-10-140-805-191	Sequence 191, App
35	49	62.0	1647	15	US-10-140-805-191	Sequence 191, App
36	49	62.0	1647	15	US-10-142-426-191	Sequence 191, App
37	49	62.0	1647	15	US-10-142-426-191	Sequence 191, App
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39	49	62.0	1675	14	US-10-146-731-135	Sequence 135, App
40	49	62.0	1675	14	US-10-146-731-135	Sequence 135, App
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43	49	62.0	1675	15	US-10-158-790-135	Sequence 135, App
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46	49	62.0	1675	15	US-10-141-759-135	Sequence 135, App
47	49	62.0	1675	15	US-10-141-759-135	Sequence 135, App
48	49	62.0	1675	15	US-10-140-805-135	Sequence 135, App
49	49	62.0	1675	15	US-10-140-805-135	Sequence 135, App
50	49	62.0	1701	14	US-10-142-426-135	Sequence 135, App
51	49	62.0	1701	14	US-10-184-644-267	Sequence 267, App
52	49	62.0	1701	14	US-10-184-644-267	Sequence 267, App
53	49	62.0	1701	13	US-10-063-665-73	Sequence 73, App
54	49	62.0	1743	14	US-10-052-586-451	Sequence 451, App
55	49	62.0	1743	14	US-10-174-590-451	Sequence 451, App
56	49	62.0	1743	14	US-10-176-758-451	Sequence 451, App
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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:25:00 ; Search time 18.5479 Seconds
(without alignments)
44.271 Million cell updates/sec

Title: US-09-124-280A-13

Perfect score: 79

Sequence: 1 CCKCKCKCKC 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	64	81.0	257 3 US-09-253-682-7	Sequence 7, Appl
5	64	81.0	257 3 US-09-527-657-7	Sequence 7, Appl
6	64	81.0	257 3 US-09-892-100-7	Sequence 7, Appl
7	54	68.4	189 4 US-09-270-767-37495	Sequence 37495, A
8	54	68.4	189 4 US-09-270-767-52712	Sequence 52712, A
9	50	63.3	13 2 US-08-850-910A-19	Sequence 19, Appl
10	50	63.3	140 4 US-09-369-247-71	Sequence 71, Appl
11	49	62.0	2123 4 US-09-949-016-7517	Sequence 7517, Ap
12	48.5	61.4	20 4 US-09-828-995B-14	Sequence 14, Appl
13	48.5	61.4	61 2 US-08-785-530-3	Sequence 3, Appl
14	48.5	61.4	61 2 US-09-123-850-3	Sequence 3, Appl
15	48.5	61.4	61 4 US-09-919-039-195	Sequence 195, Appl
16	48.5	61.4	474 4 US-09-828-995B-17	Sequence 17, Appl
17	48.5	61.4	563 4 US-09-828-995B-78	Sequence 78, Appl
18	48	60.8	1400 3 US-08-630-915A-37	Sequence 37, Appl
19	48	60.8	1917 4 US-09-627-650B-5	Sequence 5, Appl
20	48	60.8	1917 4 US-09-436-063C-5	Sequence 5, Appl
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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:43:56 / Search time 43.0851 seconds
(without alignments)
76.848 Million cell updates/sec

Title: US-09-124-280A-12
Perfect score: 52
Sequence: 1 KKKKKKPKFK 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1407402 seqs, 331100923 residues
Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database:

Published Applications AA:*

- 1: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/1/pubppa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/1/pubppa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/prodata/1/pubppa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/1/pubppa/US08_NEW_PUB.pep.*
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- 9: /cgn2_6/prodata/1/pubppa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/prodata/1/pubppa/US09B_PUBCOMB.pep.*
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- 12: /cgn2_6/prodata/1/pubppa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/prodata/1/pubppa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/prodata/1/pubppa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/prodata/1/pubppa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/1/pubppa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/prodata/1/pubppa/US10E_NEW_PUB.pep.*
- 18: /cgn2_6/prodata/1/pubppa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/prodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	52	100.0	10	US-09-124-280A-12	Sequence 12, App1
2	46	88.5	47	US-10-424-599-232807	Sequence 232807, App1
3	46	88.5	49	US-10-424-599-177679	Sequence 177679, App1
4	46	88.5	56	US-10-424-599-165415	Sequence 165415, App1
5	45	86.5	70	US-10-424-599-251180	Sequence 251180, App1
6	44	84.6	15	US-10-174-105A-191	Sequence 191, App1
7	44	84.6	20	US-09-380-682-62	Sequence 62, App1
8	44	84.6	25	US-09-999-745-42	Sequence 42, App1
9	44	84.6	25	US-09-554-000-26	Sequence 26, App1
10	44	84.6	25	US-10-857-622-46	Sequence 46, App1
11	44	84.6	70	US-10-424-599-187187	Sequence 187187, App1
12	44	84.6	389	US-10-131-410-172	Sequence 172, App1
13	43	82.7	40	US-10-424-599-238827	Sequence 238827, App1

14	43	82.7	46	US-10-437-963-127920	Sequence 127920, App1
15	43	82.7	50	US-10-424-599-193863	Sequence 193863, App1
16	43	82.7	58	US-10-424-599-168696	Sequence 168696, App1
17	43	82.7	60	US-10-424-599-196474	Sequence 196474, App1
18	43	82.7	63	US-10-424-599-191453	Sequence 191453, App1
19	43	82.7	65	US-10-424-599-236534	Sequence 236534, App1
20	43	82.7	75	US-10-424-599-151241	Sequence 151241, App1
21	43	82.7	99	US-10-437-963-137098	Sequence 137098, App1
22	43	82.7	122	US-10-424-599-214062	Sequence 214062, App1
23	43	82.7	126	US-10-437-963-173599	Sequence 173599, App1
24	43	82.7	190	US-10-437-963-157848	Sequence 157848, App1
25	42	80.8	24	US-09-999-745-43	Sequence 43, App1
26	42	80.8	24	US-09-554-000-27	Sequence 27, App1
27	42	80.8	60	US-10-437-963-187972	Sequence 187972, App1
28	42	80.8	93	US-10-437-963-163530	Sequence 163530, App1
29	42	80.8	195	US-10-171-311-121	Sequence 121, App1
30	42	80.8	195	US-10-153-666-276	Sequence 276, App1
31	42	80.8	195	US-10-153-666-396	Sequence 396, App1
32	42	80.8	247	US-09-925-302-517	Sequence 517, App1
33	42	80.8	247	US-09-925-302-517	Sequence 517, App1
34	42	80.8	247	US-09-925-302-517	Sequence 517, App1
35	41	78.8	464	US-10-282-122A-71929	Sequence 71929, App1
36	41	78.8	48	US-10-424-599-186357	Sequence 186357, App1
37	41	78.8	58	US-10-437-963-193685	Sequence 193685, App1
38	41	78.8	70	US-10-424-599-223576	Sequence 223576, App1
39	41	78.8	74	US-10-424-599-208940	Sequence 208940, App1
40	41	78.8	128	US-10-437-963-107443	Sequence 107443, App1
41	41	78.8	369	US-10-369-493-5383	Sequence 5383, App1
42	40.5	77.9	107	US-10-424-599-164613	Sequence 164613, App1
43	40	76.9	10	US-09-124-280A-42	Sequence 42, App1
44	40	76.9	56	US-10-437-963-139156	Sequence 139156, App1
45	40	76.9	58	US-10-424-599-218231	Sequence 218231, App1
46	40	76.9	60	US-10-424-599-250118	Sequence 250118, App1
47	40	76.9	65	US-10-424-599-227317	Sequence 227317, App1
48	40	76.9	69	US-10-424-599-188061	Sequence 188061, App1
49	40	76.9	72	US-10-424-599-148670	Sequence 148670, App1
50	40	76.9	79	US-10-424-599-230152	Sequence 230152, App1
51	40	76.9	79	US-10-437-963-182314	Sequence 182314, App1
52	40	76.9	80	US-10-424-599-112434	Sequence 112434, App1
53	40	76.9	85	US-10-767-701-47874	Sequence 47874, App1
54	40	76.9	86	US-10-424-599-257212	Sequence 257212, App1
55	40	76.9	92	US-10-437-963-145414	Sequence 145414, App1
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57	40	76.9	112	US-10-424-599-226452	Sequence 226452, App1
58	40	76.9	124	US-10-424-599-208858	Sequence 208858, App1
59	40	76.9	129	US-10-424-599-243357	Sequence 243357, App1
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63	39	75.0	43	US-10-424-599-246379	Sequence 246379, App1
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67	39	75.0	63	US-10-424-599-157519	Sequence 157519, App1
68	39	75.0	67	US-10-437-963-192982	Sequence 192982, App1
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70	39	75.0	116	US-10-437-963-115875	Sequence 115875, App1
71	39	75.0	121	US-10-437-963-116634	Sequence 116634, App1
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75	38	73.1	11	US-09-805-301-99	Sequence 99, App1
76	38	73.1	12	US-09-805-301-100	Sequence 100, App1
77	38	73.1	13	US-09-805-301-101	Sequence 101, App1
78	38	73.1	14	US-09-805-301-102	Sequence 102, App1
79	38	73.1	15	US-09-805-301-103	Sequence 103, App1
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82	38	73.1	18	US-09-805-301-106	Sequence 106, App1
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84	38	73.1	20	US-09-805-301-108	Sequence 108, App1
85	38	73.1	21	US-09-805-301-109	Sequence 109, App1
86	38	73.1	22	US-09-805-301-110	Sequence 110, App1
			23	US-09-805-301-111	Sequence 111, App1
			24	US-09-805-301-112	Sequence 112, App1

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OM protein - protein search, using bw model

Run on: March 26, 2005, 10:25:00 ; Search time 16.8617 Seconds

(Without alignments)
44.271 Million cell updates/sec

Title: US-09-124-280A-12

Perfect score: 52

Sequence: 1 KKKKKFKFRK 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Maximum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*
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Warning: No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
*rand is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	52	100.0	10 1	US-08-097-830E-12 Sequence 12, Appl
2	52	100.0	10 2	US-08-456-112B-12 Sequence 12, Appl
3	44	84.6	20 4	US-09-612-314A-10 Sequence 10, Appl
4	44	84.6	20 4	US-09-380-682-62 Sequence 62, Appl
5	44	84.6	25 2	US-08-818-253-26 Sequence 26, Appl
6	44	84.6	25 3	US-08-818-252-26 Sequence 26, Appl
7	44	84.6	25 3	US-08-842-322-20 Sequence 20, Appl
8	44	84.6	25 4	US-09-316-919-42 Sequence 42, Appl
9	44	84.6	25 4	US-09-316-919-42 Sequence 42, Appl
10	44	84.6	26 4	US-09-763-548B-2 Sequence 2, Appl
11	44	84.6	29 4	US-09-763-548B-1 Sequence 1, Appl
12	44	84.6	29 4	US-09-763-548B-3 Sequence 3, Appl
13	44	84.6	281 2	US-08-405-175A-9 Sequence 9, Appl
14	44	84.6	309 2	US-08-405-175A-7 Sequence 7, Appl
15	44	84.6	309 2	US-08-405-175A-8 Sequence 8, Appl
16	44	84.6	332 2	US-08-405-175A-5 Sequence 5, Appl
17	44	84.6	335 2	US-08-405-175A-6 Sequence 6, Appl
18	44	84.6	388 4	US-09-949-016-7331 Sequence 7331, Ap
19	43	82.7	163 4	US-09-270-767-38107 Sequence 38107, A
20	43	82.7	163 4	US-09-270-767-38107 Sequence 38107, A
21	42	80.8	24 2	US-08-818-253-27 Sequence 27, Appl
22	42	80.8	24 3	US-08-818-252-27 Sequence 27, Appl
23	42	80.8	24 3	US-08-818-252-21 Sequence 21, Appl
24	42	80.8	24 4	US-09-316-919-43 Sequence 43, Appl
25	42	80.8	24 4	US-09-316-919-43 Sequence 43, Appl
26	41	78.8	63 4	US-09-248-796A-23672 Sequence 23672, A
27	40	76.9	10 2	US-08-456-112B-42 Sequence 42, Appl

28	40	76.9	335 4	US-09-949-016-9033 Sequence 9033, Ap
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30	39	75.0	9 2	US-08-680-876-8 Sequence 8, Appl
31	39	75.0	9 3	US-09-263-975-8 Sequence 8, Appl
32	39	75.0	9 4	US-09-129-192C-8 Sequence 8, Appl
33	39	75.0	93 4	US-09-248-796A-23512 Sequence 23512, A
34	39	75.0	269 4	US-09-248-796A-19631 Sequence 19631, A
35	38	73.1	11 3	US-08-584-043A-98 Sequence 98, Appl
36	38	73.1	11 3	US-08-584-043A-99 Sequence 99, Appl
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38	38	73.1	13 3	US-08-584-043A-101 Sequence 101, Appl
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53	38	73.1	28 3	US-08-584-043A-116 Sequence 116, Appl
54	38	73.1	29 3	US-09-093-227-31 Sequence 31, Appl
55	38	73.1	29 3	US-09-093-227-30 Sequence 30, Appl
56	38	73.1	30 3	US-09-093-227-31 Sequence 31, Appl
57	38	73.1	30 3	US-08-584-043A-118 Sequence 118, Appl
58	38	73.1	30 3	US-09-039-780A-87 Sequence 87, Appl
59	38	73.1	31 3	US-08-584-043A-119 Sequence 119, Appl
60	38	73.1	32 3	US-08-584-043A-120 Sequence 120, Appl
61	38	73.1	33 3	US-08-584-043A-121 Sequence 121, Appl
62	38	73.1	34 3	US-08-584-043A-122 Sequence 122, Appl
63	38	73.1	35 3	US-08-584-043A-123 Sequence 123, Appl
64	38	73.1	36 3	US-08-584-043A-124 Sequence 124, Appl
65	38	73.1	36 3	US-09-039-780A-91 Sequence 91, Appl
66	38	73.1	37 3	US-08-584-043A-125 Sequence 125, Appl
67	38	73.1	38 3	US-08-584-043A-126 Sequence 126, Appl
68	38	73.1	39 3	US-08-584-043A-127 Sequence 127, Appl
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70	38	73.1	41 3	US-08-584-043A-129 Sequence 129, Appl
71	38	73.1	42 3	US-08-584-043A-130 Sequence 130, Appl
72	38	73.1	43 3	US-08-584-043A-131 Sequence 131, Appl
73	38	73.1	44 3	US-09-039-780A-88 Sequence 88, Appl
74	38	73.1	45 2	US-08-460-890A-58 Sequence 58, Appl
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82	38	73.1	67 4	US-09-107-433-4790 Sequence 4790, Ap
83	38	73.1	81 4	US-09-248-796A-27533 Sequence 27533, A
84	38	73.1	271 4	US-09-248-796A-14668 Sequence 14668, A
85	38	73.1	291 4	US-09-902-540-10710 Sequence 10710, A
86	38	73.1	1199 3	US-09-208-742-2 Sequence 2, Appl
87	38	73.1	1199 3	US-09-332-295-4 Sequence 4, Appl
88	38	73.1	1199 4	US-09-709-979-4 Sequence 4, Appl
89	38	73.1	1199 4	US-10-147-266-4 Sequence 4, Appl
90	38	73.1	36 4	US-09-463-238-26 Sequence 26, Appl
91	37	71.2	63 5	PCR-US94-01202-2 Sequence 2, Appl
92	37	71.2	66 4	US-09-248-796A-22015 Sequence 22015, A
93	37	71.2	72 4	US-09-248-796A-26208 Sequence 26208, A
94	37	71.2	75 4	US-09-248-796A-24360 Sequence 24360, A
95	37	71.2	80 4	US-09-107-532A-6963 Sequence 6963, Ap
96	37	71.2	90 4	US-09-513-993C-6871 Sequence 6871, Ap
97	37	71.2	199 2	US-08-405-175A-3 Sequence 3, Appl
98	37	71.2	200 2	US-08-405-175A-4 Sequence 4, Appl
99	37	71.2	266 4	US-09-792-024-72 Sequence 72, Appl
100	37	71.2	272 4	US-09-248-796A-15639 Sequence 15639, A

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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:43:56 ; Search time 38.7766 Seconds

(without alignments)
76.848 Million cell updates/sec

Title: US-09-124-280A-11

Perfect score: 39

Sequence: 1 KLLKLLKLL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA:*

1: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubppa/PCT_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	39	100.0	9 US-09-124-280A-11	Sequence 11, Appl
2	35	89.7	387 16 US-10-437-963-152238	Sequence 152238, A
3	34	87.2	9 14 US-10-083-259-7	Sequence 7, Appl1
4	34	87.2	9 14 US-10-109-274-7	Sequence 7, Appl1
5	34	87.2	9 15 US-10-240-641-15	Sequence 15, Appl
6	33	84.6	14 15 US-10-609-217-178	Sequence 178, Appl
7	33	84.6	14 15 US-10-632-388-178	Sequence 178, Appl
8	33	84.6	14 15 US-10-651-723-178	Sequence 178, Appl
9	33	84.6	14 15 US-10-645-761-178	Sequence 178, Appl
10	33	84.6	14 15 US-10-666-696-178	Sequence 178, Appl
11	33	84.6	14 15 US-10-653-048-178	Sequence 178, Appl
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27	32	82.1	13 14 US-10-194-686-1	Sequence 1, Appl1
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OM protein - protein search; using sw model

Run on: March 26, 2005, 10:25:00 ; Search time 15.1755 Seconds
(without alignments)
44.271 Million cell updates/sec

Title: US-09-124-280A-11

Perfect score: 39

Sequence: 1 KLKLKLKL 9

Scoring table:

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	33	84.6	11	1 US-08-465-325-94	Sequence 94, Appl
6	33	84.6	11	3 US-09-115-737-94	Sequence 94, Appl
7	33	84.6	12	1 US-08-193-521-2	Sequence 2, Appl
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9	33	84.6	12	1 US-08-465-325-95	Sequence 95, Appl
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16	33	84.6	14	1 US-08-434-120-98	Sequence 98, Appl
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97	33	84.6	21	4 US-09-726-792A-9	Sequence 9, Appl
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OM protein - protein search, using SW model

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76.848 Million cell updates/sec

Title: US-09-124-280A-10

Perfect score: 56

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Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9	51	91.1	9	9	US-09-124-280A-40
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78	36	64.3	574	9	US-09-391-340-12	Sequence 12, Appl Sequence 12, Appl
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80	36	64.3	574	9	US-09-391-340-12	Sequence 12, Appl Sequence 12, Appl
81	36	64.3	574	9	US-09-391-340-12	Sequence 12, Appl Sequence 12, Appl
82	36	64.3	574	9	US-09-391-340-12	Sequence 12, Appl Sequence 12, Appl
83	36	64.3	574	9	US-09-391-340-12	Sequence 12, Appl Sequence 12, Appl
84	36	64.3	574	9	US-09-391-340-12	Sequence 12, Appl Sequence 12, Appl
85	36	64.3	574	9	US-09-391-340-12	Sequence 12, Appl Sequence 12, Appl
86	36	64.3	574	9	US-09-391-340-12	Sequence 12, Appl Sequence 12, Appl

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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:25:00 ; Search time 16.8617 Seconds
(without alignments)
44.271 Million cell updates/sec

Title: US-09-124-280A-10
Perfect score: 56
Sequence: 1 KPRFKFKFK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	41	73.2	67	4	US-09-270-767-50968
6	40	71.4	86	4	US-09-134-000C-4858
7	39	69.6	419	4	US-09-248-796A-15450
8	38	67.9	10	1	US-08-097-830E-8
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12	38	67.9	11	1	US-08-280-397-8
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14	38	67.9	12	1	US-08-097-830E-20
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16	38	67.9	12	4	US-09-606-254-5
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22	37	66.1	77	4	US-09-328-352-7597
23	37	66.1	693	4	US-09-248-796A-26144
24	36	64.3	118	4	US-09-248-796A-28195
25	36	64.3	401	4	US-09-489-039A-8992
26	36	64.3	414	4	US-09-830-217-2
27	36	64.3	414	4	US-10-278-946-2

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29	36	64.3	574	4	US-09-391-340-12	Sequence 12, Appl
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33	35	62.5	18	4	US-09-701-588C-29	Sequence 29, Appl
34	35	62.5	18	4	US-09-747-802-65	Sequence 65, Appl
35	35	62.5	30	3	US-09-100-414B-69	Sequence 69, Appl
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37	35	62.5	30	4	US-09-770-014-69	Sequence 69, Appl
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42	35	62.5	233	4	US-09-270-767-51406	Sequence 51406, A
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56	34	60.7	78	4	US-09-107-433-2850	Sequence 2850, Ap
57	34	60.7	117	4	US-09-270-767-46330	Sequence 46330, A
58	34	60.7	117	4	US-09-270-767-61797	Sequence 61797, A
59	34	60.7	142	4	US-09-601-729-5	Sequence 5, Appl
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61	34	60.7	160	4	US-09-107-532A-3836	Sequence 3836, Ap
62	34	60.7	167	4	US-09-710-279-1802	Sequence 1802, Ap
63	34	60.7	208	4	US-09-270-767-44996	Sequence 44996, A
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68	34	60.7	403	4	US-09-248-796A-20479	Sequence 20479, A
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89	33	58.9	143	3	US-09-029-819-3	Sequence 3, Appl
90	33	58.9	143	3	US-09-102-150-8	Sequence 8, Appl
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OM protein - protein search, using SW model

Run on: March 26, 2005, 10:43:56 ; Search time 38.7766 Seconds
(without alignments)
76.848 Million cell updates/sec

Title: US-09-124-280a-9
Perfect score: 48
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Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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7	35	72.9	122	US-09-095-478-4
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16	72.9	463	10	US-09-095-478-2	Sequence 2, Appl1
17	72.9	1802	16	US-10-437-963-139865	Sequence 139865,
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19	70.8	36	14	US-10-351-641-606	Sequence 606, App
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33	70.8	438	9	US-09-908-419-2	Sequence 2, Appl1
34	70.8	438	14	US-10-056-790-2	Sequence 2, Appl1
35	70.8	438	14	US-10-056-790-36	Sequence 36, Appl
36	70.8	470	14	US-10-056-790-46	Sequence 46, Appl
37	70.8	600	9	US-09-801-368-158	Sequence 158, App
38	70.8	947	16	US-10-437-963-114679	Sequence 114679,
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44	68.8	376	15	US-10-425-114-54205	Sequence 54205, A
45	68.8	398	15	US-10-767-701-40025	Sequence 40025, A
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47	68.8	650	14	US-10-128-718-8335	Sequence 8335, Ap
48	68.8	805	16	US-10-437-963-170487	Sequence 170487,
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50	68.8	875	15	US-10-267-502-303	Sequence 303, App
51	68.8	1095	15	US-10-369-493-22025	Sequence 2025, Ap
52	68.8	1100	15	US-10-115-482-46	Sequence 46, Appl
53	66.7	36	14	US-10-351-641-608	Sequence 608, App
54	66.7	36	14	US-10-351-641-609	Sequence 609, App
55	66.7	86	16	US-10-437-963-140300	Sequence 140300,
56	66.7	262	15	US-10-424-599-284866	Sequence 284866,
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60	66.7	536	16	US-10-437-963-157400	Sequence 157400,
61	66.7	638	13	US-10-072-621-10	Sequence 10, Appl
62	66.7	666	15	US-10-267-502-309	Sequence 309, App
63	66.7	674	14	US-10-090-455-4	Sequence 4, Appl1
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OM protein - protein search, using SW model

Run on: March 26, 2005, 10:25:00 ; Search time 15.1755 seconds

(without alignments)
44.271 Million cell updates/sec

Title: US-09-124-280A-9

Perfect score: 48

Sequence: 1 RYRYRYRYV 9

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Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
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3	48	100.0	9	1	US-08-097-830E-9
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39	32	66.7	36	3	US-09-315-304B-609	Sequence 609, App
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44	32	66.7	36	4	US-09-350-641C-608	Sequence 608, App
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47	32	66.7	36	4	US-09-350-841A-609	Sequence 609, App
48	32	66.7	177	4	US-09-543-681A-4212	Sequence 4212, App
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53	31	64.6	193	4	US-09-489-039A-12557	Sequence 12557, A
54	31	64.6	250	4	US-09-813-453B-3	Sequence 3, App1
55	31	64.6	296	4	US-09-270-767-59761	Sequence 59761, A
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57	31	64.6	333	4	US-09-270-767-44340	Sequence 44340, A
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65	31	64.6	1075	4	US-09-198-452A-916	Sequence 916, App
66	31	64.6	1178	4	US-09-438-185A-851	Sequence 851, App
67	31	64.6	1422	4	US-08-469-260A-85	Sequence 85, App1
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74	30	62.5	17	4	US-09-490-324-233	Sequence 233, App
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76	30	62.5	73	4	US-09-248-796A-24970	Sequence 24970, A
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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:43:56 ; Search time 43.0851 Seconds
(without alignments)
76.848 Million cell updates/sec

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Perfect score: 50
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
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Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing filter 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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7	39	78.0	9 15 US-10-247-4768-14	Sequence 14, Appl1
8	38	76.0	10 9 US-09-124-280A-10	Sequence 10, Appl1
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16	38	76.0	66 15 US-10-424-599-152246	Sequence 152246,
17	37	74.0	248 15 US-10-424-599-165470	Sequence 265470,
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19	37	74.0	476 15 US-10-282-122A-53100	Sequence 53100, A
20	36	72.0	50 9 US-09-864-761-38298	Sequence 38298, A
21	36	72.0	114 16 US-10-767-701-56234	Sequence 56234, A
22	36	72.0	128 15 US-10-425-114-70797	Sequence 70797, A
23	36	72.0	229 16 US-10-437-963-166745	Sequence 166745,
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25	36	72.0	967 15 US-10-425-114-58755	Sequence 58755, A
26	36	72.0	967 15 US-10-425-114-62853	Sequence 62853, A
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34	35	70.0	101 15 US-10-425-114-56359	Sequence 56359, A
35	35	70.0	208 15 US-10-282-122A-45253	Sequence 45253, A
36	35	70.0	1279 15 US-09-882-227-188	Sequence 388, App
37	34	68.0	43 15 US-10-424-599-285041	Sequence 285041,
38	34	68.0	45 15 US-10-424-599-221561	Sequence 221561,
39	34	68.0	47 15 US-10-424-599-149057	Sequence 149057,
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43	34	68.0	201 15 US-10-282-122A-47069	Sequence 47069, A
44	34	68.0	230 16 US-10-437-963-104213	Sequence 104213,
45	34	68.0	243 15 US-10-425-114-63111	Sequence 46311, A
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47	34	68.0	873 15 US-10-369-493-6226	Sequence 6226, Ap
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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:25:00 ; Search time 16.8617 Seconds
(without alignments)
44.271 Million cell updates/sec

Target: US-09-124-280A-8

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Gapop 10.0, Gapext 0.5

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Maximum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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90	30	60.0	95	4	US-09-248-796A-22321	Sequence 22321, A
91	30	60.0	97	4	US-09-134-000C-1160	Sequence 1160, Ap
92	30	60.0	114	4	US-09-540-236-1979	Sequence 1979, Ap
93	30	60.0	115	4	US-09-732-210-730	Sequence 730, App
94	30	60.0	120	4	US-09-248-796A-19735	Sequence 19735, A
95	30	60.0	141	4	US-08-837-199A-24	Sequence 24, Appl
96	30	60.0	147	4	US-08-837-199A-22	Sequence 22, Appl
97	30	60.0	159	4	US-09-710-279-878	Sequence 878, App
98	30	60.0	159	4	US-09-710-279-2280	Sequence 2280, Ap
99	30	60.0	159	4	US-09-248-796A-25444	Sequence 25444, A
100	30	60.0	169	4	US-09-270-767-35406	Sequence 35406, A

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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:43:56 / Search time 30.1596 Seconds

(without alignments)
76.848 Million cell updates/sec

Title: US-09-124-280a-7

Perfect score: 35

Sequence: 1 KFLKFLK 7

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database:

Published Applications AA.*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	35	100.0	10	US-09-124-280a-8	Sequence 8, Appl
4	35	100.0	10	US-09-124-280a-41	Sequence 41, Appl
5	35	100.0	11	US-09-124-280a-37	Sequence 37, Appl
6	35	100.0	12	US-09-124-280a-20	Sequence 20, Appl
7	35	100.0	209	US-10-437-963-147868	Sequence 147868, A
8	35	100.0	476	US-10-282-122a-53100	Sequence 53100, A
9	32	91.4	66	US-10-424-599-152246	Sequence 152246, A
10	32	91.4	116	US-10-424-599-251225	Sequence 251225, A
11	32	91.4	100	US-10-607-631-10	Sequence 10, Appl
12	31	88.6	9	US-10-247-476B-13	Sequence 13, Appl
13	31	88.6	9	US-10-247-476B-14	Sequence 14, Appl

14	31	88.6	61	US-10-424-599-212895	Sequence 212895, A
15	31	88.6	785	US-10-437-963-133586	Sequence 133586, A
16	31	88.6	1012	US-10-437-963-170591	Sequence 170591, A
17	30	85.7	42	US-10-424-599-284782	Sequence 284782, A
18	30	85.7	45	US-10-029-386-29370	Sequence 29370, A
19	30	85.7	45	US-10-424-599-221561	Sequence 221561, A
20	30	85.7	65	US-10-424-599-203343	Sequence 203343, A
21	30	85.7	77	US-10-424-599-198418	Sequence 198418, A
22	30	85.7	114	US-10-767-701-56234	Sequence 56234, A
23	30	85.7	208	US-09-282-122a-45253	Sequence 45253, A
24	30	85.7	212	US-09-791-932-84	Sequence 84, Appl
25	30	85.7	228	US-10-425-114-70797	Sequence 70797, A
26	30	85.7	229	US-10-437-963-166745	Sequence 166745, A
27	30	85.7	230	US-10-437-963-104213	Sequence 104213, A
28	30	85.7	251	US-10-310-154-707	Sequence 707, Appl
29	30	85.7	289	US-10-047-676A-4	Sequence 4, Appl
30	30	85.7	309	US-09-801-368-290	Sequence 290, Appl
31	30	85.7	577	US-10-631-581-31	Sequence 31, Appl
32	30	85.7	670	US-10-032-585-7568	Sequence 7568, Appl
33	30	85.7	679	US-10-282-122a-52428	Sequence 52428, A
34	30	85.7	957	US-10-437-963-167447	Sequence 167447, A
35	30	85.7	967	US-10-425-114-58755	Sequence 58755, A
36	30	85.7	967	US-10-425-114-62853	Sequence 62853, A
37	30	85.7	967	US-10-282-122a-51805	Sequence 51805, A
38	29	82.9	18	US-10-302-547-124	Sequence 124, Appl
39	29	82.9	74	US-10-424-599-243043	Sequence 243043, A
40	29	82.9	95	US-10-424-599-159533	Sequence 159533, A
41	29	82.9	75	US-10-424-599-269978	Sequence 269978, A
42	29	82.9	181	US-10-767-701-37460	Sequence 37460, A
43	29	82.9	205	US-10-424-599-212824	Sequence 212824, A
44	29	82.9	248	US-10-424-599-265470	Sequence 265470, A
45	29	82.9	249	US-10-437-963-133560	Sequence 133560, A
46	29	82.9	262	US-10-437-963-133559	Sequence 133559, A
47	29	82.9	306	US-10-425-114-69492	Sequence 69492, A
48	29	82.9	346	US-10-425-114-56348	Sequence 56348, A
49	29	82.9	360	US-10-425-114-69594	Sequence 69594, A
50	29	82.9	461	US-10-767-701-44395	Sequence 44395, A
51	29	82.9	485	US-10-369-493-4906	Sequence 4906, Ap
52	29	82.9	536	US-10-369-493-7664	Sequence 7664, Ap
53	29	82.9	564	US-10-369-493-1706	Sequence 1706, Ap
54	29	82.9	564	US-10-369-493-2006	Sequence 2006, Ap
55	29	82.9	987	US-10-437-963-119932	Sequence 119932, A
56	29	82.9	1014	US-10-424-599-157075	Sequence 157075, A
57	29	82.9	1279	US-09-882-227-388	Sequence 388, App
58	29	82.9	2223	US-10-628-088-408	Sequence 408, App
59	28	80.0	43	US-10-424-599-285041	Sequence 285041, A
60	28	80.0	50	US-09-864-761-38298	Sequence 38298, A
61	28	80.0	63	US-10-424-599-155562	Sequence 155562, A
62	28	80.0	67	US-10-291-172-312	Sequence 312, App
63	28	80.0	67	US-10-291-172-312	Sequence 312, App
64	28	80.0	72	US-10-424-599-213192	Sequence 213192, A
65	28	80.0	73	US-10-264-049-21302	Sequence 21302, Ap
66	28	80.0	83	US-10-424-599-265486	Sequence 265486, A
67	28	80.0	102	US-10-424-599-265104	Sequence 265104, A
68	28	80.0	106	US-10-291-172-688	Sequence 688, App
69	28	80.0	116	US-10-221-278-688	Sequence 688, App
70	28	80.0	112	US-10-424-599-155874	Sequence 155874, A
71	28	80.0	115	US-10-425-114-68048	Sequence 68048, A
72	28	80.0	250	US-10-234-432-25	Sequence 25, Appl
73	28	80.0	257	US-09-670-406A-53	Sequence 53, Appl
74	28	80.0	257	US-10-159-901-53	Sequence 53, Appl
75	28	80.0	279	US-10-402-894A-10	Sequence 10, Appl
76	28	80.0	279	US-10-424-599-249309	Sequence 249309, A
77	28	80.0	288	US-10-264-437-2368	Sequence 2368, Ap
78	28	80.0	321	US-09-989-723-36	Sequence 36, Appl
79	28	80.0	321	US-09-989-723-36	Sequence 36, Appl
80	28	80.0	321	US-09-989-729-36	Sequence 36, Appl
81	28	80.0	321	US-09-989-727-36	Sequence 36, Appl
82	28	80.0	321	US-09-989-711-36	Sequence 36, Appl
83	28	80.0	321	US-09-989-732-36	Sequence 36, Appl
84	28	80.0	321	US-09-991-073-36	Sequence 36, Appl
85	28	80.0	321	US-09-990-442-36	Sequence 36, Appl
86	28	80.0	321	US-09-991-163-36	Sequence 36, Appl

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OM protein - protein search, using SW model

Run on: March 26, 2005, 10:25:00 / Search time 11.8032 Seconds
(without alignments)
44.271 Million cell updates/sec

Title: US-09-124-280a-7

Perfect score: 35
Sequence: 1 KFLKFLK 7

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database:

Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	35	100.0	7	2	US-08-456-112B-7
5	35	100.0	7	2	US-08-456-112B-38
6	35	100.0	10	1	US-08-097-830E-8
7	35	100.0	10	2	US-08-456-112B-8
8	35	100.0	10	2	US-08-456-112B-41
9	35	100.0	11	1	US-08-049-871-8
10	35	100.0	11	1	US-07-819-893-8
11	35	100.0	11	1	US-08-280-397-8
12	35	100.0	11	2	US-08-456-112B-37
13	35	100.0	12	1	US-08-097-830E-20
14	35	100.0	12	2	US-08-456-112B-20
15	32	91.4	138	4	US-09-270-767-36351
16	32	91.4	138	4	US-09-270-767-51568
17	30	85.7	113	4	US-09-732-210-1231
18	30	85.7	114	4	US-09-540-236-1979
19	30	85.7	151	3	US-09-134-001C-5595
20	30	85.7	157	4	US-09-710-279-1802
21	30	85.7	219	4	US-09-583-110-5079
22	30	85.7	225	4	US-09-328-352-6504
23	30	85.7	289	3	US-09-627-376-4
24	30	85.7	289	4	US-10-047-676B-4
25	30	85.7	323	4	US-09-328-352-7120
26	30	85.7	360	4	US-09-949-016-10589
27	30	85.7	373	4	US-09-489-039A-8389

28	30	85.7	376	4	US-09-248-796A-16143	Sequence 16143, A
29	30	85.7	403	4	US-09-248-796A-14239	Sequence 14239, A
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32	29	82.9	208	4	US-09-248-796A-20557	Sequence 20557, A
33	29	82.9	323	4	US-09-248-796A-16328	Sequence 16328, A
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38	28	80.0	97	4	US-09-134-000C-4160	Sequence 4160, Ap
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58	27	77.1	9	2	US-08-456-112B-40	Sequence 40, Appl
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62	27	77.1	58	4	US-09-621-976-7068	Sequence 7068, Ap
63	27	77.1	63	4	US-09-107-532A-7158	Sequence 7158, Ap
64	27	77.1	65	4	US-09-248-796A-24449	Sequence 24449, A
65	27	77.1	74	4	US-09-248-796A-25664	Sequence 25664, A
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74	27	77.1	207	4	US-09-270-767-34523	Sequence 34523, A
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78	27	77.1	249	4	US-09-248-796A-27561	Sequence 27561, A
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82	27	77.1	318	4	US-09-585-858-43	Sequence 43, Appl
83	27	77.1	318	4	US-10-270-878-43	Sequence 43, Appl
84	27	77.1	339	4	US-09-692-570-6	Sequence 6, Appl1
85	27	77.1	347	3	US-08-445-515-58	Sequence 58, Appl
86	27	77.1	348	3	US-08-445-515-56	Sequence 56, Appl
87	27	77.1	378	4	US-09-107-532A-4777	Sequence 4777, Ap
88	27	77.1	400	4	US-09-198-453A-102	Sequence 302, App
89	27	77.1	400	4	US-09-438-188A-291	Sequence 291, App
90	27	77.1	420	5	US-08-588-258B-40	Sequence 40, Appl
91	27	77.1	420	5	PCR-US96-08285-40	Sequence 40, Appl
92	27	77.1	438	4	US-09-248-796A-19601	Sequence 19601, A
93	27	77.1	546	4	US-09-248-796A-10455	Sequence 20455, A
94	27	77.1	550	4	US-09-328-352-5277	Sequence 5277, Ap
95	27	77.1	550	4	US-09-248-796A-25337	Sequence 25337, A
96	27	77.1	610	4	US-09-248-796A-17030	Sequence 17030, A
97	27	77.1	617	4	US-09-198-452A-135	Sequence 155, App
98	27	77.1	617	4	US-09-438-185A-138	Sequence 138, App
99	27	77.1	758	4	US-09-248-796A-16107	Sequence 16107, A
100	27	77.1	808	4	US-09-543-661A-4995	Sequence 4995, Ap

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OM protein - protein search, using SW model

Run on: March 26, 2005, 10:43:56 ; Search time 30.1596 Seconds
(without alignments)

76.848 Million cell updates/sec

Title: US-09-124-280a-6

Perfect score: 34

Sequence: 1 KFLKXTL 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	7	US-09-124-280a-6	Sequence 6, Appl1
2	31	91.2	176	US-10-437-963-107635	Sequence 107635, Appl1
3	30	88.2	6	US-09-124-280a-32	Sequence 32, Appl1
4	30	88.2	10	US-09-124-280a-36	Sequence 36, Appl1
5	30	88.2	36	US-10-424-599-227949	Sequence 227949, Appl1
6	30	88.2	59	US-09-989-890-188	Sequence 188, Appl1
7	30	88.2	59	US-10-424-599-227949	Sequence 227949, Appl1
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OW protein - protein search, using SW model

Run on: March 26, 2005, 10:25:00 / Search time 11.8032 Seconds

(without alignments)
44.271 Million cell updates/sec

Title: US-09-124-280a-6

Perfect score: 34

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Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	31	91.2	383	4	US-09-248-796A-16746
5	30	88.2	6	1	US-08-049-871-3
6	30	88.2	6	1	US-07-819-893-3
7	30	88.2	6	1	US-08-280-397-3
8	30	88.2	6	1	US-08-037-830E-30
9	30	88.2	6	2	US-08-456-112B-32
10	30	88.2	10	1	US-08-049-871-7
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13	30	88.2	10	1	US-08-218-026-48
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38	28	82.4	890	4	US-09-546-013-18	Sequence 18, Appl
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56	27	79.4	503	3	US-09-068-195-24	Sequence 24, Appl
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77	26	76.5	151	4	US-09-270-767-42527	Sequence 42527, A
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94	26	76.5	326	4	US-09-543-681A-5565	Sequence 5565, Ap
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96	26	76.5	332	4	US-09-583-117B-16	Sequence 3964, Ap
97	26	76.5	351	1	US-08-468-847B-14	Sequence 16, Appl
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OM protein - protein search, using ew model

Run on: March 26, 2005, 10:43:56 ; Search time 43.0851 Seconds

(without alignments)
76.848 Million cell updates/sec

Title: US-09-124-280A-5

Perfect score: 55

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Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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7	41	74.5	178	15	US-10-424-599-231286
8	40	72.7	20	9	US-09-778-200-30
9	40	72.7	20	14	US-10-192-832-33
10	39	70.9	93	16	US-10-437-963-118223
11	38	69.1	68	15	US-10-424-599-173645
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31	63.6	1741	10	US-10-197-824-111	Sequence 111, App
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49	61.8	497	5	US-10-425-563-16	Sequence 16, App1
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52	61.8	852	13	US-10-011-588-25	Sequence 25, App1
53	61.8	852	9	US-09-255-829-22	Sequence 22, App1
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55	61.8	860	14	US-10-241-596-22	Sequence 22, App1
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57	61.8	862	14	US-10-241-596-94	Sequence 94, App1
58	61.8	862	14	US-10-241-596-171	Sequence 171, App
59	61.8	862	14	US-10-241-596-173	Sequence 173, App
60	61.8	864	14	US-10-241-596-102	Sequence 102, App
61	61.8	865	14	US-10-241-596-100	Sequence 100, App
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63	61.8	866	14	US-10-241-596-104	Sequence 104, App
64	61.8	867	14	US-10-241-596-80	Sequence 80, App1
65	61.8	867	14	US-10-241-596-96	Sequence 96, App1
66	61.8	867	14	US-10-241-596-96	Sequence 96, App1
67	61.8	870	14	US-10-241-596-92	Sequence 92, App1
68	61.8	871	14	US-10-241-596-84	Sequence 84, App1
69	61.8	871	14	US-10-241-596-86	Sequence 86, App1
70	61.8	871	14	US-10-241-596-90	Sequence 90, App1
71	61.8	876	14	US-10-241-596-82	Sequence 82, App1
72	61.8	876	14	US-10-241-596-106	Sequence 106, App
73	61.8	876	14	US-10-241-596-108	Sequence 108, App
74	61.8	888	14	US-10-241-596-112	Sequence 112, App
75	61.8	1169	9	US-09-255-829-20	Sequence 20, App1
76	61.8	1169	14	US-10-241-596-20	Sequence 20, App1
77	61.8	1290	15	US-10-452-024-119	Sequence 119, App
78	61.8	1291	15	US-10-354-174-40	Sequence 40, App1
79	61.8	1291	15	US-10-354-174-42	Sequence 42, App1
80	61.8	1291	15	US-10-271-012-42	Sequence 42, App1
81	61.8	1291	15	US-10-271-012-42	Sequence 42, App1
82	61.8	1291	15	US-10-452-024-117	Sequence 117, App1
83	61.8	1291	15	US-10-452-024-118	Sequence 118, App
84	61.8	1291	15	US-10-452-024-118	Sequence 118, App
85	61.8	1291	15	US-10-452-024-121	Sequence 121, App

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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:25:00 ; Search time 16.8617 Seconds

(without alignments)
44.271 Million cell updates/sec

Title: US-09-124-280A-5

Perfect score: 55

Sequence: 1 KKKKKKKFKF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summariesDatabase : Issued Patents AA.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	55	100.0	10	1	US-08-097-8308-5
2	55	100.0	10	2	US-08-456-112B-5
3	44	80.0	10	2	US-08-456-112B-5
4	41	74.5	10	1	US-08-097-8308-15
5	41	74.5	10	2	US-08-456-112B-15
6	41	74.5	150	4	US-09-270-767-46076
7	40	72.7	92	4	US-09-270-767-58304
8	40	72.7	435	4	US-09-270-767-42976
9	38	69.1	359	4	US-09-270-767-61061
10	38	69.1	475	4	US-09-270-767-45548
11	37	67.3	64	4	US-09-248-796A-25040
12	37	67.3	76	4	US-09-248-796A-21442
13	36	65.5	212	4	US-09-270-767-39848
14	36	65.5	212	4	US-09-270-767-55065
15	36	65.5	911	4	US-09-107-433-4987
16	35	63.6	180	4	US-09-248-796A-26726
17	35	63.6	271	4	US-09-270-767-35990
18	35	63.6	271	4	US-09-270-767-51207
19	34	61.8	70	4	US-09-248-796A-27957
20	34	61.8	100	4	US-09-621-976-4475
21	34	61.8	387	4	US-09-270-767-45451
22	34	61.8	858	4	US-09-255-829-24
23	34	61.8	858	4	US-09-255-829-22
24	34	61.8	858	4	US-09-255-829-20
25	33	60.0	33	4	US-09-270-767-41242
26	33	60.0	33	4	US-09-270-767-56458
27	33	60.0	33	4	US-09-270-767-56458

28	33	60.0	108	4	US-09-583-110-4267	Sequence 4267, Ap
29	33	60.0	117	4	US-09-270-767-41032	Sequence 41032, A
30	33	60.0	117	4	US-09-270-767-56248	Sequence 56248, A
31	33	60.0	120	4	US-09-107-433-2947	Sequence 2947, Ap
32	33	60.0	168	4	US-09-270-767-44708	Sequence 44708, A
33	33	60.0	395	4	US-09-491-577-98	Sequence 98, Appl
34	33	60.0	826	4	US-09-248-796A-14704	Sequence 14704, A
35	33	60.0	1022	4	US-09-949-016-8864	Sequence 8864, Ap
36	33	60.0	1022	4	US-09-949-016-9041	Sequence 9041, Ap
37	33	60.0	2470	4	US-08-265-967C-2	Sequence 2, Appl1
38	33	60.0	2470	4	US-08-305-790B-3	Sequence 88, Appl1
39	32	58.2	28	4	US-09-674-973A-88	Sequence 91, Appl1
40	32	58.2	29	4	US-09-674-973A-89	Sequence 92, Appl1
41	32	58.2	37	4	US-09-674-973A-91	Sequence 25935, A
42	32	58.2	38	4	US-09-248-796A-25935	Sequence 57748, A
43	32	58.2	62	4	US-09-270-767-57748	Sequence 22981, A
44	32	58.2	63	4	US-09-248-796A-22981	Sequence 26570, A
45	32	58.2	74	4	US-09-248-796A-26570	Sequence 59867, A
46	32	58.2	87	4	US-09-270-767-459867	Sequence 3804, Ap
47	32	58.2	102	3	US-09-134-001C-3804	Sequence 27032, A
48	32	58.2	116	4	US-09-248-796A-27012	Sequence 42453, A
49	32	58.2	139	4	US-09-270-767-42453	Sequence 61784, A
50	32	58.2	239	4	US-09-270-767-61784	Sequence 42680, A
51	32	58.2	295	4	US-09-270-767-61784	Sequence 5891, Ap
52	32	58.2	421	4	US-09-328-352-5891	Sequence 46218, A
53	32	58.2	502	4	US-09-270-767-36832	Sequence 36832, A
54	32	58.2	553	4	US-09-270-767-55049	Sequence 52049, A
55	32	58.2	614	4	US-09-248-796A-16106	Sequence 16106, A
56	32	58.2	614	4	US-09-248-796A-18382	Sequence 18382, A
57	32	58.2	642	4	US-09-270-767-44442	Sequence 44442, A
58	32	58.2	682	4	US-09-270-767-44433	Sequence 12, Appl
59	32	58.2	733	4	US-08-097-8308-12	Sequence 56594, A
60	32	58.2	1032	10	US-09-107-533A-5704	Sequence 5704, Ap
61	31	56.4	10	2	US-09-270-767-41473	Sequence 41473, A
62	31	56.4	97	4	US-09-270-767-41489	Sequence 41889, A
63	31	56.4	104	4	US-09-270-767-41489	Sequence 38485, A
64	31	56.4	121	4	US-09-270-767-53702	Sequence 37033, A
65	31	56.4	142	4	US-09-270-767-53250	Sequence 52250, A
66	31	56.4	195	4	US-09-270-767-34886	Sequence 34886, A
67	31	56.4	277	4	US-09-270-767-34886	Sequence 50103, A
68	31	56.4	277	4	US-09-270-767-34886	Sequence 32839, A
69	31	56.4	277	4	US-09-270-767-34886	Sequence 15655, A
70	31	56.4	277	4	US-09-270-767-34886	Sequence 15169, A
71	31	56.4	289	4	US-08-135-510-5	Sequence 5, Appl1
72	31	56.4	289	4	US-08-483-852-5	Sequence 5, Appl1
73	31	56.4	289	4	US-08-483-852-5	Sequence 5, Appl1
74	31	56.4	358	4	US-08-477-953-5	Sequence 5, Appl1
75	31	56.4	358	4	US-08-477-953-5	Sequence 15011, A
76	31	56.4	404	4	US-09-248-796A-15011	Sequence 28, Appl
77	31	56.4	451	4	US-08-135-511-28	Sequence 3, Appl1
78	31	56.4	482	1	US-08-483-852-3	Sequence 8, Appl1
79	31	56.4	482	1	US-08-483-852-3	Sequence 18, Appl
80	31	56.4	482	1	US-08-483-852-3	Sequence 10802, A
81	31	56.4	482	1	US-08-483-852-3	Sequence 41568, A
82	31	56.4	482	1	US-08-483-852-3	Sequence 43370, A
83	31	56.4	482	1	US-08-483-852-3	Sequence 4036, Ap
84	31	56.4	482	1	US-08-483-852-3	Sequence 4843, Ap
85	31	56.4	482	1	US-08-483-852-3	Sequence 27725, A
86	31	56.4	482	1	US-08-483-852-3	Sequence 19, Appl
87	31	56.4	482	1	US-08-483-852-3	Sequence 57136, A
88	31	56.4	482	1	US-08-483-852-3	Sequence 95, Appl
89	31	56.4	482	1	US-08-483-852-3	
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OM protein - protein search, using SW model

Run on: March 26, 2005, 10:43:56 ; Search time 43.0851 Seconds

(without alignments)
76.848 Million cell updates/sec

Title: US-09-124-280a-4

Perfect score: 55
Sequence: 1 KDXDKDXDKD 10Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Seatched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database :

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6: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	10	US-09-124-280a-4	Sequence 4, Appl1
2	55	100.0	201	US-10-425-114-70425	Sequence 70425, A
3	55	100.0	216	US-10-425-114-68080	Sequence 68080, A
4	55	100.0	459	US-10-767-701-45450	Sequence 45450, A
5	55	100.0	899	US-10-437-963-122313	Sequence 122313, A
6	51	92.7	218	US-10-425-114-64096	Sequence 64096, A
7	51	92.7	257	US-10-225-065A-714	Sequence 714, App
8	51	92.7	257	US-10-374-780A-1992	Sequence 1992, App
9	51	92.7	257	US-10-412-699B-1768	Sequence 1768, App
10	51	92.7	488	US-10-108-260A-3519	Sequence 3519, App
11	49	89.1	151	US-10-263-828-81	Sequence 81, Appl
12	49	89.1	294	US-10-424-599-237559	Sequence 237559, A
13	49	89.1	580	US-10-424-599-237561	Sequence 237561, A

14	48	87.3	160	US-10-424-599-249584	Sequence 249584, A
15	48	87.3	205	US-10-424-599-267199	Sequence 267199, A
16	48	87.3	273	US-10-437-963-190100	Sequence 190100, A
17	47	85.5	94	US-10-767-701-32420	Sequence 32420, A
18	47	85.5	257	US-10-424-599-281202	Sequence 281202, A
19	47	85.5	941	US-10-032-585-7930	Sequence 7930, App
20	47	85.5	1259	US-10-032-585-7120	Sequence 7120, App
21	46	83.6	268	US-10-437-963-203813	Sequence 203813, A
22	46	83.6	373	US-10-408-765A-1630	Sequence 1630, App
23	46	83.6	566	US-10-437-963-203809	Sequence 203809, A
24	46	83.6	1566	US-10-177-223-366	Sequence 366, App
25	46	83.6	1566	US-10-437-963-30	Sequence 30, Appl1
26	46	83.6	1566	US-10-425-970-2	Sequence 2, Appl1
27	45	81.8	110	US-10-424-599-218536	Sequence 218536, A
28	45	81.8	413	US-10-425-114-68652	Sequence 68652, A
29	45	81.8	558	US-10-437-963-103757	Sequence 103757, A
30	45	81.8	1020	US-10-267-502-398	Sequence 398, App
31	44	80.0	514	US-10-104-047-2661	Sequence 2661, App
32	44	80.0	540	US-10-276-774-1724	Sequence 1724, App
33	44	80.0	624	US-10-105-959-4	Sequence 4, Appl1
34	44	80.0	624	US-10-258-662-20	Sequence 20, Appl1
35	44	80.0	752	US-10-003-295-2	Sequence 2, Appl1
36	44	80.0	752	US-10-660-763-2	Sequence 2, Appl1
37	44	80.0	822	US-10-003-295-4	Sequence 4, Appl1
38	44	80.0	822	US-10-660-763-4	Sequence 4, Appl1
39	44	80.0	928	US-10-108-605-261	Sequence 261, App
40	44	80.0	1257	US-10-369-493-6761	Sequence 6761, App
41	44	80.0	1487	US-10-437-963-161300	Sequence 161300, A
42	43	78.2	35	US-10-043-344-67	Sequence 67, Appl1
43	43	78.2	36	US-10-043-344-66	Sequence 66, Appl1
44	43	78.2	200	US-10-767-701-63004	Sequence 43004, A
45	43	78.2	212	US-10-425-114-57740	Sequence 57740, A
46	43	78.2	349	US-09-925-297-644	Sequence 644, App
47	43	78.2	385	US-10-437-963-132764	Sequence 132764, A
48	43	78.2	529	US-10-043-344-150	Sequence 150, App
49	43	78.2	547	US-10-043-344-149	Sequence 149, App
50	43	78.2	600	US-10-424-599-154043	Sequence 154043, A
51	43	78.2	644	US-10-043-344-6	Sequence 6, Appl1
52	43	78.2	647	US-10-043-344-148	Sequence 148, App
53	43	78.2	660	US-10-043-344-8	Sequence 8, Appl1
54	43	78.2	660	US-10-043-344-10	Sequence 10, Appl1
55	43	78.2	911	US-10-437-963-112571	Sequence 112571, A
56	42	76.4	117	US-10-767-701-62725	Sequence 62725, A
57	42	76.4	136	US-10-342-224-106	Sequence 106, App
58	42	76.4	184	US-10-424-599-248564	Sequence 248564, A
59	42	76.4	205	US-10-437-963-116057	Sequence 116057, A
60	42	76.4	237	US-10-282-122A-44787	Sequence 44787, A
61	42	76.4	260	US-10-425-114-45558	Sequence 45558, A
62	42	76.4	261	US-10-424-599-272329	Sequence 272329, A
63	42	76.4	362	US-10-403-571-156	Sequence 156, App
64	42	76.4	573	US-10-437-963-104679	Sequence 104679, A
65	42	76.4	633	US-10-425-114-56709	Sequence 56709, A
66	42	76.4	734	US-10-437-963-168478	Sequence 168478, A
67	42	76.4	865	US-10-060-065-4	Sequence 4, Appl1
68	42	76.4	1027	US-10-205-219-123	Sequence 123, App
69	42	76.4	1266	US-09-757-781-63	Sequence 63, Appl1
70	42	76.4	1266	US-09-931-969A-2	Sequence 2, Appl1
71	42	76.4	1356	US-10-079-699-2	Sequence 2, Appl1
72	42	76.4	1356	US-09-757-781-2	Sequence 2, Appl1
73	41	74.5	95	US-10-424-599-247580	Sequence 247580, A
74	41	74.5	119	US-10-767-701-26710	Sequence 26710, A
75	41	74.5	209	US-10-767-701-39778	Sequence 39778, A
76	41	74.5	287	US-10-121-209-910	Sequence 10, Appl1
77	41	74.5	287	US-10-121-209-16	Sequence 16, Appl1
78	41	74.5	287	US-10-131-539-26	Sequence 26, Appl1
79	41	74.5	287	US-10-131-539-26	Sequence 26, Appl1
80	41	74.5	306	US-10-424-599-228613	Sequence 228613, A
81	41	74.5	356	US-10-437-963-159634	Sequence 159634, A
82	41	74.5	459	US-10-425-114-596107	Sequence 596107, A
83	41	74.5	665	US-09-820-243A-107	Sequence 107, App
84	41	74.5	765	US-09-882-274-2	Sequence 2, Appl1
85	41	74.5	765	US-10-408-765A-1119	Sequence 1119, App
86	41	74.5	765	US-10-484-577-679	Sequence 679, App

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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:25:00 ; Search time 16.8617 Seconds
(without alignments)
44.271 Million cell updates/sec

Title: US-09-124-280A-4
Perfect score: 55
Sequence: 1 KDKXDKDKD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	10	US-08-456-112B-4	Sequence 4, Appl1
2	55	100.0	422	US-09-270-767-46208	Sequence 46208, A
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4	55	100.0	635	US-09-248-796A-16944	Sequence 16944, A
5	51	92.7	54	US-09-270-767-58902	Sequence 58902, A
6	51	92.7	63	US-09-270-767-58546	Sequence 58546, A
7	51	92.7	282	US-09-270-767-43536	Sequence 43536, A
8	51	92.7	478	US-09-270-767-43204	Sequence 43204, A
9	48	87.3	71	US-09-248-796A-24829	Sequence 24829, A
10	48	87.3	207	US-09-248-796A-14709	Sequence 14709, A
11	47	85.5	819	US-09-248-796A-15758	Sequence 15758, A
12	46	83.6	1566	US-09-581-472B-2	Sequence 2, Appl1
13	46	83.6	1581	US-09-110-517-2	Sequence 2, Appl1
14	45	81.8	315	US-09-248-796A-18003	Sequence 18003, A
15	45	81.8	417	US-09-252-991A-20650	Sequence 20650, A
16	44	80.0	274	US-09-270-767-43153	Sequence 43153, A
17	44	80.0	491	US-09-248-796A-19540	Sequence 19540, A
18	44	80.0	541	US-09-248-796A-18318	Sequence 18318, A
19	44	80.0	752	US-09-817-180-2	Sequence 2, Appl1
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21	44	80.0	822	US-09-817-180-4	Sequence 4, Appl1
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23	44	80.0	822	US-09-538-092-866	Sequence 866, App
24	43	78.2	35	US-08-487-890A-67	Sequence 67, Appl1
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49	43	78.2	547	US-08-483-577A-149	Sequence 149, App
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51	43	78.2	547	US-08-649-518-149	Sequence 149, App
52	43	78.2	644	US-08-487-890A-148	Sequence 148, App
53	43	78.2	644	US-08-478-435-6	Sequence 148, App
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55	43	78.2	644	US-08-478-373-6	Sequence 148, App
56	43	78.2	644	US-08-474-671-6	Sequence 148, App
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64	43	78.2	657	US-08-613-009A-18	Sequence 18, App
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88	42	76.4	1312	US-09-335-689-2	Sequence 43669, A
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91	41	74.5	285	US-09-248-796A-14945	Sequence 14945, A
92	41	74.5	300	US-09-395-689-1	Sequence 19450, A
93	41	74.5	363	US-09-248-796A-15286	Sequence 1, Appl1
94	41	74.5	363	US-08-860-3688-20	Sequence 1286, A
95	41	74.5	455	US-09-270-767-44339	Sequence 20, Appl1
96	41	74.5	518	US-09-248-796A-19845	Sequence 44339, A
97	41	74.5	755	US-08-663-112-2	Sequence 19845, A
98	41	74.5	765	US-08-663-112-2	Sequence 2, Appl1
99	41	74.5	765	US-09-538-092-906	Sequence 906, App
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			1	US-08-188-582-20	Sequence 20, Appl1

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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:43:56 / Search time 43.0851 Seconds
(without alignments)
76.848 Million cell updates/sec

Title: US-09-124-280A-1
Perfect score: 50
Sequence: 1 KKKKKKKKKK 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1407402 seqs, 331100923 residues
Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database:

Published Applications AA:*

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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
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- 14: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	50	100.0	10	15	US-10-366-493-95
5	50	100.0	10	16	US-10-650-435-13
6	50	100.0	10	17	US-10-652-295-10
7	50	100.0	11	9	US-09-933-708-19
8	50	100.0	11	9	US-09-933-708-19
9	50	100.0	11	15	US-10-156-527-5
10	50	100.0	11	15	US-10-156-527-12
11	50	100.0	11	16	US-10-755-082-11
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13	50	100.0	12	9	US-09-805-301-100

14	50	100.0	12	14	US-10-075-869-96	Sequence 96, App1
15	50	100.0	12	15	US-10-366-493-96	Sequence 96, App1
16	50	100.0	12	16	US-10-650-435-14	Sequence 14, App1
17	50	100.0	13	9	US-09-805-301-7	Sequence 7, App1
18	50	100.0	13	9	US-09-805-301-45	Sequence 45, App1
19	50	100.0	13	9	US-09-805-301-101	Sequence 101, App1
20	50	100.0	13	14	US-10-243-836-9	Sequence 9, App1
21	50	100.0	14	8	US-08-910-386A-53	Sequence 53, App1
22	50	100.0	14	9	US-09-933-708-10	Sequence 10, App1
23	50	100.0	14	9	US-09-805-301-8	Sequence 8, App1
24	50	100.0	14	9	US-09-805-301-46	Sequence 46, App1
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33	50	100.0	15	14	US-10-108-844-11	Sequence 11, App1
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37	50	100.0	16	9	US-09-805-301-48	Sequence 48, App1
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39	50	100.0	16	15	US-10-226-879-19	Sequence 19, App1
40	50	100.0	17	9	US-09-805-301-11	Sequence 11, App1
41	50	100.0	17	9	US-09-805-301-49	Sequence 49, App1
42	50	100.0	17	9	US-09-805-301-105	Sequence 105, App1
43	50	100.0	17	14	US-10-312-691-7	Sequence 7, App1
44	50	100.0	18	9	US-09-805-301-12	Sequence 12, App1
45	50	100.0	18	9	US-09-805-301-50	Sequence 50, App1
46	50	100.0	18	9	US-09-805-301-106	Sequence 106, App1
47	50	100.0	19	9	US-09-805-301-51	Sequence 51, App1
48	50	100.0	19	9	US-09-805-301-13	Sequence 13, App1
49	50	100.0	19	9	US-09-805-301-107	Sequence 107, App1
50	50	100.0	19	10	US-09-911-569-10	Sequence 10, App1
51	50	100.0	19	14	US-10-157-021-190	Sequence 190, App1
52	50	100.0	19	14	US-10-200-879-10	Sequence 10, App1
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86	50	100.0	25	9	US-09-805-301-19	Sequence 19, App1

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OM protein - protein search, using sw model

Run on: March 26, 2005, 10:25:00 ; Search time 16.8617 Seconds

(without alignments)
44.271 Million cell updates/sec

Title: US-09-124-280A-1

Perfect score: 50

Sequence: 1 KKKKKKKKKK 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	50	100.0	11	1	US-07-694-983-15
5	50	100.0	12	3	US-08-584-043A-44
6	50	100.0	12	3	US-08-584-043A-100
7	50	100.0	13	3	US-08-584-043A-7
8	50	100.0	13	3	US-08-584-043A-45
9	50	100.0	13	3	US-08-584-043A-101
10	50	100.0	14	3	US-08-584-043A-8
11	50	100.0	14	3	US-08-584-043A-46
12	50	100.0	14	3	US-08-584-043A-102
13	50	100.0	15	3	US-08-584-043A-9
14	50	100.0	15	3	US-08-584-043A-47
15	50	100.0	15	3	US-08-584-043A-103
16	50	100.0	15	3	US-09-120-653D-30
17	50	100.0	15	3	US-09-050-811-6
18	50	100.0	15	3	US-09-050-811-11
19	50	100.0	16	3	US-08-584-043A-10
20	50	100.0	16	3	US-08-584-043A-48
21	50	100.0	16	3	US-08-584-043A-104
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23	50	100.0	17	3	US-08-584-043A-49
24	50	100.0	17	3	US-08-584-043A-105
25	50	100.0	18	3	US-08-584-043A-12
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72	50	100.0	26	4	US-09-424-656-3	Sequence 4, App1
73	50	100.0	27	3	US-08-836-786-4	Sequence 4, App1
74	50	100.0	27	3	US-08-584-043A-21	Sequence 21, App1
75	50	100.0	27	3	US-08-584-043A-59	Sequence 59, App1
76	50	100.0	27	3	US-08-584-043A-115	Sequence 115, App1
77	50	100.0	27	4	US-09-424-656-2	Sequence 2, App1
78	50	100.0	27	4	US-09-424-656-4	Sequence 4, App1
79	50	100.0	28	3	US-08-584-043A-22	Sequence 22, App1
80	50	100.0	28	3	US-08-584-043A-60	Sequence 60, App1
81	50	100.0	28	3	US-08-584-043A-116	Sequence 116, App1
82	50	100.0	28	4	US-09-424-656-1	Sequence 1, App1
83	50	100.0	29	3	US-08-584-043A-23	Sequence 23, App1
84	50	100.0	29	3	US-08-584-043A-61	Sequence 61, App1
85	50	100.0	29	3	US-08-584-043A-117	Sequence 117, App1
86	50	100.0	30	1	US-08-097-830B-2	Sequence 2, App1
87	50	100.0	30	2	US-08-456-112B-2	Sequence 2, App1
88	50	100.0	30	2	US-08-584-043A-24	Sequence 24, App1
89	50	100.0	30	3	US-08-584-043A-62	Sequence 62, App1
90	50	100.0	30	3	US-08-584-043A-118	Sequence 118, App1
91	50	100.0	30	3	US-09-039-780A-87	Sequence 87, App1
92	50	100.0	30	3	US-09-050-811-9	Sequence 9, App1
93	50	100.0	30	4	US-09-530-560B-45	Sequence 45, App1
94	50	100.0	31	3	US-08-584-043A-25	Sequence 25, App1
95	50	100.0	31	3	US-08-584-043A-63	Sequence 63, App1
96	50	100.0	31	3	US-08-584-043A-119	Sequence 119, App1
97	50	100.0	31	3	US-09-039-780A-116	Sequence 116, App1
98	50	100.0	32	3	US-09-426-680-25	Sequence 25, App1
99	50	100.0	32	3	US-08-584-043A-26	Sequence 26, App1
100	50	100.0	32	3	US-08-584-043A-64	Sequence 64, App1